

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 23, 2001, 06:11:10 ; Search time 10.2 Seconds
(without alignments)
755.636 Million cell updates/sec

Title: US-09-559-764-1

Perfect score.: 1198

Sequence: 1 IVGGKRRPQPFLASTON.....VALFRDWIDGVLNPPGGPA 225

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

1 number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 1198 | 100.0 | 251 | 1 CAP7_HUMAN | P20160 homo sapien |
| 2 | 772 | 64.4 | 219 | 1 CAP7_PIG | P80015 sus scrofa |
| 3 | 500 | 41.7 | 267 | 1 ELNE_HUMAN | P08246 homo sapien |
| 4 | 476.5 | 39.8 | 256 | 1 PRN3_HUMAN | P24158 homo sapien |
| 5 | 333 | 27.8 | 245 | 1 MCT1_SHEEP | P80931 ovis aries |
| 6 | 333 | 27.8 | 262 | 1 GRAA_HUMAN | P12544 homo sapien |
| 7 | 331.5 | 27.7 | 226 | 1 DDN1_BOVIN | P80219 bos taurus |
| 8 | 331.5 | 27.7 | 248 | 1 TRY1_CHICK | O90627 gallus gall |
| 9 | 331 | 27.6 | 247 | 1 MCT2_RAT | P00770 rattus norv |
| 10 | 329.5 | 27.5 | 257 | 1 GRAM_HUMAN | P51124 homo sapien |
| 11 | 327.5 | 27.3 | 248 | 1 TRY2_CHICK | O90628 gallus gall |
| 12 | 327 | 27.3 | 253 | 1 CFAD_HUMAN | P00746 homo sapien |
| 13 | 326 | 27.2 | 258 | 1 GRAK_RAT | P49864 rattus norv |
| 14 | 325 | 27.1 | 246 | 1 MCT9_MOUSE | O35164 mus musculus |
| 15 | 325 | 27.1 | 245 | 1 MCTX_MOUSE | O00356 mus musculus |
| 16 | 323.5 | 27.0 | 259 | 1 CFAD_MOUSE | P03953 mus musculus |
| 17 | 323 | 27.0 | 259 | 1 CFAD_PIG | P51779 sus scrofa |
| 18 | 321 | 26.8 | 246 | 1 MCT1_MOUSE | P11034 mus musculus |
| 19 | 320.5 | 26.8 | 261 | 1 CATG_MOUSE | P28293 mus musculus |
| 20 | 320 | 26.7 | 246 | 1 MCT4_RAT | P97592 rattus norv |
| 21 | 320 | 26.7 | 245 | 1 GRAC_MOUSE | P08882 mus musculus |
| 22 | 318.5 | 26.6 | 255 | 1 CATG_HUMAN | P08311 homo sapien |
| 23 | 317 | 26.5 | 245 | 1 MCT4_MOUSE | P21812 mus musculus |
| 24 | 315.5 | 26.3 | 247 | 1 GRAB_MOUSE | P04187 mus musculus |
| 25 | 314 | 26.2 | 251 | 1 MCT3_SHEEP | O46683 ovis aries |
| 26 | 313.5 | 26.2 | 263 | 1 GRAB_MOUSE | O35205 mus musculus |
| 27 | 310.5 | 25.9 | 261 | 1 KLK3_MACMU | P33619 macaca mula |
| 28 | 310 | 25.9 | 244 | 1 MCT2_MOUSE | P15119 mus musculus |
| 29 | 310 | 25.9 | 260 | 1 MCT1_RAT | P09650 rattus norv |
| 30 | 309.5 | 25.8 | 263 | 1 CFAD_RAT | P32038 rattus norv |
| 31 | 309 | 25.8 | 248 | 1 NKPI_RAT | P18291 rattus norv |
| 32 | 308 | 25.7 | 248 | 1 GRAB_MOUSE | P08883 mus musculus |
| 33 | 307.5 | 25.7 | 251 | 1 KLKE_HUMAN | O9p0g3 homo sapien |

RESULT 1

| ID | CAP7_HUMAN | STANDARD; | PRT; | 251 AA. |
|----|---|-----------|------|---------|
| AC | P20160; P80014; | | | |
| DT | 01-FEB-1991 (Rel. 17, Created) | | | |
| DT | 01-OCT-1993 (Rel. 27, Last sequence update) | | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | | |
| DE | AZUROCIDIN PRECURSOR (CATIONIC ANTIMICROBIAL PROTEIN CAP37) | | | |
| DE | (HEPARIN-BINDING PROTEIN) (HBP). | | | |
| GN | AZUL. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=92013155; PubMed=1919011; | | | |
| RA | Morgan J.G., Sukienicki T., Pereira H.A., Spitznagel J.K., | | | |
| RA | Guerra M.E., Larrick J.L.; | | | |
| RT | "Cloning of the cDNA for the serine protease homolog | | | |
| RT | CAP37/azurocidin, a microbicidal and chemotactic protein from human | | | |
| RT | granulocytes." | | | |
| RL | J. Immunol. 147:3210-3214(1991). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=92390417; PubMed=1518849; | | | |
| RA | Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P., | | | |
| RA | Jenne D.E.; | | | |
| RT | "Three human elastase-like genes coordinately expressed in the | | | |
| RT | myelomonocyte lineage are organized as a single genetic locus on | | | |
| RT | 19pter." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., | | | |
| RA | Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S., | | | |
| RA | Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J., | | | |
| RA | Danagan L., Poundstone P., Christensen M., Georgescu A., Avila J., | | | |
| RA | Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G., | | | |
| RA | Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., | | | |
| RA | Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Frong S., | | | |
| RA | Kobayashi A., Olsen A.S., Carrano A.V.; | | | |
| RL | Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [4] | | | |
| RP | SEQUENCE OF 3-251 FROM N.A. | | | |
| RC | TISSUE=Neutrophils; | | | |
| RX | MEDLINE=91264832; PubMed=2049091; | | | |
| RA | Almeida R.P., Melchior M., Campanelli D., Nathan C., Gabay J.E.; | | | |
| RT | "Complementary DNA sequence of human neutrophil azurocidin, an | | | |
| RT | antibiotic with extensive homology to serine proteases." | | | |
| RL | Biochem. Biophys. Res. Commun. 177:688-695(1991). | | | |
| RN | [5] | | | |
| RP | SEQUENCE OF 27-248. | | | |
| RX | MEDLINE=91032128; PubMed=2226832; | | | |
| RA | Pohl J., Ferreira H.A., Martin N.M., Spitznagel J.K.; | | | |
| RT | "Amino acid sequence of CAP37, a human neutrophil granule-derived | | | |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 306.5 | 25.6 | 248 | 1 | MCT8_RAT | P97594 rattus norv |
| 35 | 306.5 | 25.6 | 264 | 1 | GRAK_HUMAN | P49863 homo sapien |
| 36 | 306 | 25.5 | 254 | 1 | KLK4_HUMAN | O9V5K2 homo sapien |
| 37 | 305.5 | 25.5 | 244 | 1 | TRY2_XENLA | P70059 xenopus lae |
| 38 | 305.5 | 25.5 | 261 | 1 | KLK3_HUMAN | P07288 homo sapien |
| 39 | 304.5 | 25.4 | 238 | 1 | TRY3_SALSA | P35033 salmo salar |
| 40 | 303.5 | 25.3 | 239 | 1 | KLK2_CAVPO | P12323 cavia porce |
| 41 | 303.5 | 25.3 | 250 | 1 | TRYP_PLEPL | P35034 pleuronecte |
| 42 | 303.5 | 25.3 | 260 | 1 | KLK8_HUMAN | O60259 homo sapien |
| 43 | 303 | 25.3 | 246 | 1 | GRAH_HUMAN | P20718 homo sapien |
| 44 | 303 | 25.3 | 248 | 1 | GRL1_RAT | O06605 rattus norv |
| 45 | 302.5 | 25.3 | 260 | 1 | GRAA_MOUSE | P11032 mus musculu |

ALIGNMENTS

RT antibacterial and monocyte-specific chemotactic glycoprotein
 RT structurally similar to neutrophil elastase.;
 RL FEBS Lett. 272:200-204(1990).
 RN [16]
 RC SEQUENCE OF 27-248.
 RP TISSUE-Neutrophils;
 RX MEDLINE=91224149; PubMed=2026172;
 RA Flodgaard H., Oestergaard E., Bayne S., Jendensen A., Thomsen J.,
 RA Engels M., Wollmer A.;
 RT "Covalent structure of two novel neutrophil leucocyte-derived
 RT proteins of porcine and human origin. Neutrophil elastase homologues
 RT with strong monocyte and fibroblast chemotactic activities.";
 RL Eur. J. Biochem. 197:535-547(1991).
 RN [17]
 RP SEQUENCE OF 27-47.
 RX MEDLINE=91378304; PubMed=1897955;
 RA Green B.G., Weston H., Ashe B.M., Doherty J., Finke P., Hagemann W.,
 RA Lark M., Mao J., Maycock A., Moore V., Rutherford R., Shah S.,
 RA Walakavits L., Knight W.B.;
 RT "PMN elastases: a comparison of the specificity of human isozymes and
 RT the enzyme from other species toward substrates and inhibitors.";
 RL Arch. Biochem. Biophys. 286:284-292(1991).
 RN [18]
 RP SEQUENCE OF 27-46.
 RX MEDLINE=89315847; PubMed=2501794;
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
 RA Marra M.N., Seeger M., Nathan C.F.;
 RT "Antibiotic proteins of human polymorphonuclear leukocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
 RN [19]
 RP SEQUENCE OF 27-46 AND 194-217.
 RX MEDLINE=90130450; PubMed=2404977;
 RA Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;
 RT "Characterization of two azurophilic granule proteases with active-site
 RT homology to neutrophil elastase.";
 RL J. Biol. Chem. 265:2038-2041(1990).
 RN [10]
 RP SEQUENCE OF 27-67.
 RC TISSUE-Neutrophils;
 RX MEDLINE=90157837; PubMed=2406527;
 RA Pereira H.A., Spitznagel J.K., Pohl J., Wilson D.E., Morgan J.,
 RA Palings I., Larrick J.W.;
 RT "CAP 37, a 37 kd human neutrophil granule cationic protein shares
 RT homology with inflammatory proteinases.";
 RL Life Sci. 46:189-196(1990).
 RN [11]
 RP SEQUENCE OF 27-68.
 RC TISSUE-Neutrophils;
 RX MEDLINE=90237224; PubMed=2332502;
 RA Pereira H.A., Shafer W.M., Pohl J., Morgan J., Spitznagel J.K.;
 RT "CAP37, a human neutrophil-derived chemotactic factor with monocyte
 RT specific activity.";
 RL J. Clin. Invest. 85:1468-1476(1990).
 RN [12]
 RP REVIEW.
 RX MEDLINE=92095171; PubMed=1755383;
 RA Morgan J.G., Pereira H.A., Sukiennicki L., Spitznagel J.K.,
 RA Larrick J.W.;
 RT "Human neutrophil granule cationic protein CAP37 is a specific
 RT macrophage chemotaxin that shares homology with inflammatory
 RT proteinases.";
 RL Adv. Exp. Med. Biol. 305:89-96(1991).
 RN [13]
 RP SYNTHESIS OF 46-70.
 RX MEDLINE=93281653; PubMed=8506327;
 RA Pereira H.A., Erdem I., Pohl J., Spitznagel J.K.;
 RT "Synthetic bactericidal peptide based on CAP37: a 37-kDa human
 RT neutrophil granule-associated cationic antimicrobial protein
 RT chemotactic for monocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4733-4737(1993).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=97249288; PubMed=9095193;

RA Iversen L.F., Kastrup J.S., Bjoern S.E., Rasmussen P.B., Wiberg F.C.,
 RA Flodgaard H.J., Larsen I.K.;
 RT "Structure of HBP, a multifunctional protein with a serine proteinase
 RT fold.";
 RL Nat. Struct. Biol. 4:265-268(1997).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (1.12 ANGSTROMS).
 RX MEDLINE=98437573; PubMed=9761855;
 RA Karlsen S., Iversen L.F., Larsen I.K., Flodgaard H.J., Kastrup J.S.;
 RT "Atomic resolution structure of human HBP/CAP37/azurocidin.";
 RL Acta Crystallogr. D 54:598-609(1998).
 CC -!- FUNCTION: THIS IS A NEUTROPHIL GRANULE-DERIVED ANTIBACTERIAL AND
 CC MONOCYTE- AND FIBROBLAST-SPECIFIC CHEMOTACTIC GLYCOPROTEIN. BINDS
 CC HEPARIN. THE CYTOTOXIC ACTION IS LIMITED TO MANY SPECIES OF GRAM-
 CC NEGATIVE BACTERIA; THIS SPECIFICITY MAY BE EXPLAINED BY A STRONG
 CC AFFINITY OF THE VERY BASIC N-TERMINAL HALF FOR THE NEGATIVELY
 CC CHARGED LIPOPOLYSACCHARIDES THAT ARE UNIQUE TO THE GRAM-NEGATIVE
 CC BACTERIAL OUTER ENVELOPE. IT MAY PLAY A ROLE IN MEDIATING
 CC RECRUITMENT OF MONOCYTES IN THE SECOND WAVE OF INFLAMMATION.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. ELASTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M96326; AAB59353.1; -;
 CC EMBL; X58794; CAA41601.1; -;
 CC EMBL; AC004799; AAC18957.1; -;
 CC PIR; A46455; TRHAZ;
 CC PIR; A46268; A46268;
 CC PDB; 1AE5; 1I-MAR-98.
 CC PDB; 1A7S; 23-MAR-99.
 CC MEROPS; S01.971; -;
 CC MIM; 162815; -;
 CC InterPro; IPR001254; -;
 CC InterPro; IPR001314; -;
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 CC PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
 CC Serine protease homology; Glycoprotein; Chemotaxis; Antibiotic;
 CC Heparin-binding; Signal; 3D-structure.
 CC SIGNAL 1 26
 CC CHAIN 27 248 AZUROCIDIN.
 CC PROPEP 249 251
 CC DOMAIN 46 70
 CC DOMAIN 52 84
 CC CARBOHYD 126 126
 CC CARBOHYD 140 140
 CC CARBOHYD 171 171
 CC DISULFID 52 68
 CC DISULFID 149 207
 CC DISULFID 180 186
 CC DISULFID 197 222
 CC VARIANT 248 248
 CC MUTAGEN 52 52
 CC MUTAGEN 68 68
 CC CONFLICT 36 36
 CC CONFLICT 130 130
 CC SEQUENCE 251 AA; 26885 MW; 22F80D9EBE87DE60 CRC64;
 FT SQ
 FT MISSING (IN 50% OF THE MOLECULES).
 FT /FTID=VAR.006496.
 FT C->S: LOSS OF ANTIBIOTIC ACTIVITY.
 FT C->S: LOSS OF ANTIBIOTIC ACTIVITY.
 FT S -> H (IN REF. 9).
 FT S -> N (IN REF. 6).
 FT
 Query Match 100.0%; Score 1198; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 6.2e-104;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: November 23, 2001, 06:10:39 ; Search time 17.17 seconds
(without alignments)
998.210 Million cell updates/sec

Title: US-09-559-764-1

Perfect score: 1198
Sequence: 1 IGVGKARPPFPFLASIQN.....VALFRDWIDGLVNNPQGP 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

T number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 1198 | 100.0 | 251 | 1 TRHUAZ | azurocidin precurs |
| 2 | 772 | 64.4 | 219 | 1 TRPGAZ | azurocidin - pig |
| 3 | 500 | 41.7 | 267 | 1 ELHUL | leukocyte elastase |
| 4 | 481.5 | 40.2 | 256 | 1 PRHU3 | proteinase 3 (EC 3 |
| 5 | 471.5 | 39.4 | 265 | 2 I48679 | neutrophil elastas |
| 6 | 333 | 27.8 | 262 | 1 A31372 | duodenase - bovine |
| 7 | 331.5 | 27.7 | 226 | 2 S69370 | granzyme A (EC 3.4 |
| 8 | 331 | 27.6 | 247 | 1 PRRTG | mast cell proteina |
| 9 | 329.5 | 27.5 | 249 | 2 A55634 | granzyme M (EC 3.4 |
| 10 | 328 | 27.4 | 248 | 2 S43259 | granzyme-like prot |
| 11 | 327.5 | 27.3 | 248 | 2 S55067 | trypsin (EC 3.4.21 |
| 12 | 327 | 27.3 | 244 | 2 A34910 | mast cell proteina |
| 13 | 326 | 27.2 | 256 | 2 I56220 | trypsin 2 - rat |
| 14 | 325 | 27.1 | 246 | 1 DBHU | complement factor |
| 15 | 325 | 27.0 | 246 | 2 A38678 | mast cell proteina |
| 16 | 323.5 | 27.0 | 259 | 1 WNM528 | complement factor |
| 17 | 321 | 26.8 | 261 | 1 A46504 | chymase (EC 3.4.21 |
| 18 | 320.5 | 26.8 | 261 | 2 S40162 | cathepsin G (EC 3. |
| 19 | 320 | 26.7 | 248 | 1 PRMSC2 | granzyme C (EC 3.4 |
| 20 | 318.5 | 26.6 | 255 | 2 A27122 | cathepsin G (EC 3. |
| 21 | 317 | 26.5 | 246 | 2 B38678 | mast cell proteina |
| 22 | 316 | 26.4 | 244 | 2 S26042 | chymase (EC 3.4.21 |
| 23 | 315.5 | 26.3 | 247 | 1 PRMSC1 | granzyme B (EC 3.4 |
| 24 | 314.5 | 26.3 | 250 | 2 T01779 | trypsin (EC 3.4.21 |
| 25 | 314 | 26.2 | 226 | 2 JE0151 | myonase (EC 3.4. - |
| 26 | 314 | 26.2 | 251 | 2 T10262 | mast cell serine p |
| 27 | 310.5 | 25.9 | 261 | 1 S35711 | seminogelase (EC 3 |
| 28 | 310 | 25.9 | 244 | 2 A46721 | chymase (EC 3.4.21 |
| 29 | 310 | 25.9 | 251 | 2 JC2125 | chymase (EC 3.4.21 |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 309.5 | 25.8 | 263 | 1 I55608 | complement factor |
| 31 | 309 | 25.8 | 248 | 2 A43520 | natural killer cel |
| 32 | 308 | 25.7 | 248 | 1 S01007 | granzyme F (EC 3.4 |
| 33 | 306.5 | 25.6 | 264 | 2 S65663 | granzyme 3 (EC 3.4 |
| 34 | 305.5 | 25.5 | 261 | 1 A32297 | seminogelase (EC 3 |
| 35 | 304.5 | 25.4 | 238 | 2 S31779 | trypsin (EC 3.4.21 |
| 36 | 303.5 | 25.3 | 239 | 2 A27207 | tissue kallikrein |
| 37 | 303.5 | 25.3 | 250 | 2 S31384 | trypsin (EC 3.4.21 |
| 38 | 303 | 25.3 | 246 | 2 A32692 | cytotoxic T-lympho |
| 39 | 303 | 25.3 | 248 | 2 S33755 | granzyme-like prot |
| 40 | 302.5 | 25.3 | 257 | 2 B45061 | granzyme A (EC 3.4 |
| 41 | 302.5 | 25.3 | 260 | 2 A45061 | granzyme A (EC 3.4 |
| 42 | 300 | 25.0 | 232 | 1 KQPG | tissue kallikrein |
| 43 | 300 | 25.0 | 246 | 2 S64707 | chymase (EC 3.4.21 |
| 44 | 299.5 | 25.0 | 243 | 2 A35871 | trypsin (EC 3.4.21 |
| 45 | 297 | 24.8 | 242 | 2 S49489 | trypsin (EC 3.4.21 |

ALIGNMENTS

RESULT 1

TRHUAZ
azurocidin precursor [validated] - human
N:Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neu
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000
C:Accession: A46268; A46455; S16450; S18520; S12881; S15445; S14738; B33913; A60708;
R:Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992
A:Title: Three human elastase-like genes coordinately expressed in the myelomonocyte
A:Reference number: A46268; MUID:923390417
A:Accession: A46268
A:Molecule type: DNA
A:Residues: 1-251 <ZIM>
A:Cross-references: GB:M96326; NID:q179301; PIDN:AAB59353.1; PID:q179302
A:Note: sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:1128
R:Morgan, J.G.; Sukiennicki, T.; Pereira, H.A.; Spitznagel, J.K.; Guerra, M.E.; Larri
J. Immunol. 147, 3210-3214, 1991
A:Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a micr
A:Reference number: A46455; MUID:92013155
A:Accession: A46455
A:Molecule type: mRNA
A:Residues: 1-251 <MOR>
A:Cross-references: GB:M96326; NID:q179301; PIDN:AAB59353.1; PID:q179302
A:Note: sequence extracted from NCBI backbone (NCBIN:60386, NCBI:P60395)
R:Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabay, J.E.
Biochem. Biophys. Res. Commun. 177, 688-695, 1991
A:Title: Complementary DNA sequence of human neutrophil azurocidin, an antibiotic wit
A:Reference number: S16450; MUID:91264832
A:Accession: S16450
A:Molecule type: mRNA
A:Residues: 3-251 <ALM>
A:Cross-references: EMBL:X58794; NID:g28976; PIDN:CAA41601.1; PID:g28977
A:Accession: S18520
A:Molecule type: protein
A:Residues: 47-51, 'S', 53-59, 'T', 61-62, 'V', 64-87 <AL2>
R:Pohl, J.; Pereira, H.A.; Martin, N.M.; Spitznagel, J.K.
FEBS Lett. 272, 200-204, 1990
A:Title: Amino acid sequence of CAP37, a human neutrophil granule-derived antibacteri
A:Reference number: S12881; MUID:91032128
A:Accession: S12881
A:Molecule type: protein
A:Residues: 27-248 <POH>
R:Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wo
Eur. J. Biochem. 197, 535-547, 1991
A:Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of po
A:Reference number: S15393; MUID:91224149
A:Accession: S15445
A:Molecule type: protein
A:Residues: 27-129, 'N', 131-247 <FLO>
A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 6 in having 190-

R:Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; Ma Arch. Biochem. Biophys. 286, 284-292, 1991
A:Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme
A:Reference number: S14736; MUID:91378304
A:Accession: S14738
A:Molecule type: protein
A:Residues: 27-47 <GRE>
R:Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989
A:Title: Antibiotic proteins of human polymorphonuclear leukocytes.
A:Reference number: A33913; MUID:89315847
A:Accession: B33913
A:Molecule type: protein
A:Residues: 27-46 <GAB>
R:Perreira, H.A.; Shafer, W.M.; Pohl, J.; Martens, L.E.; Spitznagel, J.K. J. Clin. Invest. 85, 1468-1476, 1990
A:Title: CAP37, a human neutrophil-derived chemotactic factor with monocyte specific activity
A:Reference number: A60708; MUID:90237224
A:Accession: A60708
A:Molecule type: protein
A:Residues: 27-68 <PER>
R:Wojcik, K.R.; Skubitz, K.M.; Gray, B.H. Infect. Immun. 59, 4193-4200, 1991
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which are
A:Reference number: A43600; MUID:92040097
A:Accession: B43600
A:Molecule type: protein
A:Residues: 27-48 <WAS>
R:Miyauchi, K.T.; Bodeau, A.L. Infect. Immun. 60, 4973-4975, 1992
A:Title: Human neutrophil azurocidin synergizes with leukocyte elastase and cathepsin G
A:Reference number: A49211; MUID:93014226
A:Accession: A49211
A:Molecule type: protein
A:Residues: 27-46 <MIY>
R:Shelldard, J.E.; Leitch, H.A.; Logan, P.M.; Masters, W.R.; Levy, J.G. Exp. Hematol. 19, 136-142, 1991
A:Title: Purification of an in vitro inhibitor of normal myelopoiesis using a monoclonal
A:Reference number: A61502; MUID:91122218
A:Accession: A61502
A:Molecule type: protein
A:Residues: 27-48 <SHE>
R:Wilde, C.G.; Snable, J.E.; Griffith, J.E.; Scott, R.W. J. Biol. Chem. 265, 2038-2041, 1990
A:Title: Characterization of two azurophilic granule proteases with active-site homology
A:Reference number: A43981; MUID:90130450
A:Accession: B43981
A:Molecule type: protein
A:Residues: 27-35, 'H', 37-46; 194-217 <WIL>
R:Perreira, H.A.; Spitznagel, J.K.; Pohl, J.; Wilson, D.E.; Morgan, J.; Palings, I.; Larr Life Sci. 46, 189-196, 1990
A:Title: CAP 37, a 37 kD human neutrophil granule cationic protein shares homology with
A:Reference number: PH0081; MUID:90157837
A:Accession: PH0081
A:Molecule type: protein
A:Residues: 27-67 <PE2>
A:Experimental source: polymorphonuclear leukocyte
C:Comment: This protein is homologous to several proteinases but lacks proteolytic activity
C:Genetics: microbial activity against a number of gram-negative bacteria.
A:Gene: GDB:AZU1
A:Cross-references: GDB:135033; OMIM:162815
A:Map position: 19p13.3-19p13.3
A:Introns: 20/1; 72/2; 150/3; 198/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; inflammation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-26/Domain: amino-terminal propeptide #status predicted <PRO>
F:27-246/Product: azurocidin #status experimental
F:27-239/Domain: trypsin homology <TRY>
F:67, 115, 201/Region: defective catalytic triad
F:249-251/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:52-68/Disulfide bonds: #status experimental
F:126-140, 171/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:149-207, 180-186, 197-222/Disulfide bonds: #status predicted
Query Match 100.0%; Score 1198; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-102;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
DB 27 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 86
QY 61 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 120
DB 87 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 146
QY 121 TRCQVAGWGQSQRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 180
DB 147 TRCQVAGWGQSQRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 206
QY 181 CEGLAHGVASFSLGPGCGPDEFTRVALFRDWIDGVLNNPGCPGA 225
DB 207 CEGLAHGVASFSLGPGCGPDEFTRVALFRDWIDGVLNNPGCPGA 251
RESULT 2
TRPGANZ
A:Alternate names: heparin-binding protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jul-1997
C:Accession: S15393
R:Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wo Eur. J. Biochem. 197, 535-547, 1991
A:Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of po
A:Reference number: S15393; MUID:91224149
A:Accession: S15393
A:Molecule type: protein
A:Residues: 1-219 <FLO>
R:Sorensen, H.H.; Thomsen, J.; Bayne, S.; Hojrup, P.; Roepstorff, P. Biomed. Environ. Mass Spectrom. 19, 713-720, 1990
A:Title: Strategies for determination of disulphide bridges in proteins using plasma
A:Reference number: A37448; MUID:91167744
A:Contents: annotation; disulfide bonds
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein
F:1-211/Domain: trypsin homology <TRY>
F:41,88,173/Region: defective catalytic triad
F:26-42,122-179,152-158/Disulfide bonds: #status experimental
F:113,144/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 64.4%; Score 772; DB 1; Length 219;
Best Local Similarity 68.6%; Pred. No. 4.1e-63;
Matches 151; Conservative 26; Mismatches 41; Indels 2; Gaps 2;
QY 1 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
DB 1 IVGGRRAQPQEPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
QY 61 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 120
DB 61 ROOE-OSRQTFSSISQNGYDPRONLNDVLLQLDREALTSPVLPQNATVEAG 119
QY 121 TRCQVAGWGQSQRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 180
DB 120 TNCQVAGWGQRLRLRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 178
QY 181 CEGLAHGVASFSLGPGCGPDEFTRVALFRDWIDGVLNNP 220
DB 179 CNGLAOGVASFLLRRRRSSGFFTRVALFRNWDVSLNPP 218

| Result No. | Query % | | | DB | ID | Description |
|------------|---------|-------|--------|----|--------|---------------------|
| | Score | Match | Length | | | |
| 1 | 510.5 | 42.6 | 254 | 11 | O08809 | O08809 mus musculus |
| 2 | 510.5 | 42.6 | 254 | 11 | O61096 | O61096 mus musculus |
| 3 | 473.5 | 39.5 | 258 | 6 | Q9GME1 | Q9GME1 ornithorhyn |
| 4 | 471.5 | 39.4 | 265 | 11 | O61515 | O61515 mus musculus |
| 5 | 355.5 | 29.7 | 200 | 4 | Q9UQ88 | Q9UQ88 homo sapien |
| 6 | 352 | 29.4 | 207 | 11 | Q9Z284 | Q9Z284 mus musculus |
| 7 | 344 | 28.7 | 248 | 5 | O16126 | O16126 boltenia vi |
| 8 | 328 | 27.4 | 239 | 6 | Q9GME0 | Q9GME0 ornithorhyn |
| 9 | 328 | 27.4 | 246 | 11 | Q9EP80 | Q9EP80 mus musculus |
| 10 | 328 | 27.4 | 248 | 11 | O63224 | O63224 rattus norv |
| 11 | 324 | 27.0 | 248 | 11 | O63636 | O63636 rattus norv |
| 12 | 324 | 27.0 | 251 | 6 | Q9GLN2 | Q9GLN2 bos taurus |
| 13 | 323 | 27.0 | 247 | 11 | O70500 | O70500 rattus norv |
| 14 | 316 | 26.4 | 239 | 11 | Q9EQ72 | Q9EQ72 mus musculus |
| 15 | 316 | 26.4 | 246 | 11 | Q9EP09 | Q9EP09 mus musculus |
| 16 | 313.5 | 26.2 | 256 | 11 | O9R0K0 | O9R0K0 mus musculus |
| 17 | 306 | 25.5 | 233 | 4 | Q9GZL6 | Q9GZL6 homo sapien |
| 18 | 305 | 25.5 | 254 | 6 | Q9XSN6 | Q9XSN6 sus scrofa |
| 19 | 304.5 | 25.4 | 269 | 5 | Q9V929 | Q9V929 drosophila |

Db 30 I VGGHEARPHSRPYVASLQLSRFFGSHFCGGTLIHPRFVLTAAHCL

Query Match 42.6%; Score 510.5; DB 11; Length 254;
Best Local Similarity 47.1%; Pred. No. 1e-42;
Matches 107; Conservative 35; Mismatches 78; Indels 7; Gaps 4;

| | | | |
|--------|---|--------------------------------------|------------------------------|
| QY | 58 | YDLRRRERQSROTFTSISSSENSGYDPOONLNDLMF | OLDREANTSSVTILPLPQNATV 117 |
| Df | 90 | HDLTSLSEPE-QOKFTISQVFQNNYNPEENLDVL | OLNRTASLGKEVASLASLPQQDTL 148 |
| QY | 118 | EAGTRCQAVAGVSQRSGGLRFEPFVNVTTPES | CRPNNVCTGVLTRRGICNGDGGT 177 |
| Df | 149 | SQGTQCGLAWGRGLGTQAFTPRVLQELINVTV-T | CREHNVCTLVPRRAAGICFGDSGG 207 |
| QY | 178 | PLVCEGLAHGVASFSLGPCG--RGPDFDFTRVALFF | WIDGVLNNPFG 222 |
| Df | 208 | P LICNGILHGVDSEFVIRECASLQFPDEFARYSMY | WIONVLRLGAEP 254 |
| RESULT | 2 | | |
| Q61096 | | | |
| ID | Q61096 | PRELIMINARY; | PRT; 254 AA. |
| AC | A61096; | | |
| DT | 01-NOV-1996 (TreeBLrel. 01, Created) | | |
| DT | 01-AUG-1999 (TreeBLrel. 11, Last sequence update) | | |
| DT | 01-MAR-2001 (TreeBLrel. 16, Last annotation update) | | |
| DR | PROTEINASE-3 (PROTEINASE 3) (PRE-PRO-PROCESSING PTN3). | | |
| GN | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; | | |
| OX | NCBI_TaxID=10090; | | |
| XX | [1] | | |
| R | SEQUENCE FROM N.A. | | |
| RC | STRAIN=129SVJ; | | |
| RA | Sturck A., Franklin K.F., Wu S.Q., Hoshino T. | | |
| RT | "Characterization and localization of the gene for mouse proteinase-3 and neutrophil elastase"; | | |
| RT | Submitted (AUG-1998) to the EMBL/GenBank databases. | | |
| RL | [2] | | |
| RP | SEQUENCE OF 2-254 FROM N.A. | | |
| RC | STRAIN=BALB/C; | | |
| RX | MEDLINE=97362044; PubMed=9211743; | | |
| RA | Aveskog M., Lutzelichwab C., Huang M.R. | | |
| RT | "Characterization of cDNA clones encoding myeloblastine and cathepsin G"; | | |
| RL | Immunogenetics 46:181-191(1997). | | |
| CC | -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY. | | |
| CC | -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (sl). | | |
| DR | EMBL; AF082186; AAC79701.1; -. | | |
| DR | EMBL; U43525; AAB67271.1; -. | | |
| DR | HSP; P20160; IAE5. | | |
| DR | MEROFS; S01.134; -. | | |
| DR | MGD; MG1.893580; Prtn3. | | |
| D | InterPro; IPR001254; -. | | |
| D | InterPro; IPR001314; -. | | |
| DR | Pfam; PF00089; trypsin; l. | | |
| DR | PRINTS; PR00722; CHYMOTRYPSIN. | | |
| DR | PROSITE; PS00134; TRYPsin_HIS; UNKNOWN | | |
| DR | PROSITE; PS00135; TRYPsin_SER; l. | | |
| DR | SMART; SM00020; Tryp_Spc; l. | | |
| KW | Hydrolase; Protease; Serine protease. | | |
| SO | SEQUENCE . 254 AA; 27626 MW; 00CEB989CB79CA CRC64; | | |

| | Query Match | 42.6% | Score 510.3 | DB 11; | Length 254; |
|----|-----------------------|-----------------------------------|-----------------------------|-----------|-------------|
| | Best Local Similarity | 47.1% | Pred. No. 39-42; | | |
| | Matches 107; | Conservative 35; | Mismatches 72; | Indels 7; | Gaps 4; |
| Qy | 1 | IVGGRKARPPFPFLASTQNCQ--GRHFCGGAL | AREVMTAAASCFQSONPCGVSTVVLGA | 57 | |
| | | : : : : : | | | |
| Db | 30 | IVGGEARPHSRPYVASLQLSRFPSCHEGCTLA | PREVLTAACHLQDISWQLTVVVLGA | 89 | |
| | | : : : : : | | | |
| Qy | 58 | YDLRRERQSGRTFTGISMSENGYPDQONLDLM | LQLDREANLTSSVTIILPLPQNAIV | 117 | |
| | | : : : : : | | | |
| Db | 90 | HPDLLSSEPE-QQKFTISQVFQNNYPNEENLDV | LQLNRTASLKGKAVASLPPQDQTL | 148 | |
| | | : : : : : | | | |
| Qy | 118 | EAGTRCQVAGWSQSGGRLSRFPFRFVNVTVTPE | DCRPNNVCTGVLTFRRGICNGDGGT | 177 | |
| | | : : : : : | | | |

| | | | |
|--------|--|---|---------------------------|
| Db | 149 | SQGTQCLAMGWRGLGTQATPRVLQELNVTV--TFLCREHNVTCLVPRRAAGTCFGDSGG | 2020 |
| Qy | 178 | PLVCEGLHGVASFSGLGPCG--RGPDPFFTRVALFRWDIGVLNNPGP | 222 |
| Db | 208 | PLICNGILHGVDSFVIRECASLQFPDPFFARVSMYVDWIQNLVLRGAEP | 254 |
| | | : : : :: | |
| RESULT | 3 | | |
| Q9GME1 | ID | Q9GME1 | PRELIMINARY; PRT; 258 AA. |
| AC | Q9GME1: | | |
| DT | 01-MAR-2001 | (TrEMBLrel. 16, Created) | |
| DT | 01-MAR-2001 | (TrEMBLrel. 16, Last sequence update) | |
| DT | 01-MAR-2001 | (TrEMBLrel. 16, Last annotation update) | |
| DE | N-ELASTASE. | | |
| OS | Ornithorhynchus anatinus (Duckbill platypus). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus. | | |
| OX | NCBI_TaxID=9258; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Poorafshar M.M., Hellman L.L.; | | |
| RA | "Identification and structural analysis of three serine proteases in | | |
| RT | monotreme, platypus, ornithorhynchus anatinus." | | |
| RL | Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AF275652; AAG00451.1; - | | |
| SC | SEQUENCE 258 AA; 28165 MW; 2E1752C300A36138 CRC64; | | |

[illegible]

| RESULT | 4 | |
|--------|--|---|
| Q61515 | | |
| ID | Q61515 | PREJUTINARY; PRT; 265 AA. |
| AC | Q61515; | |
| DT | 01-NOV-1996 | (TREMBLrel. 01, Created) |
| DT | 01-NOV-1996 | (TREMBLrel. 01, Last sequence update) |
| DT | 01-MAR-2001 | (TREMBLrel. 16, Last annotation update) |
| DE | NEUTROPHIL ELASTASE; | |
| OS | Mus musculus (Mouse). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; | |
| OX | NCBI_TaxID:10090; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RC | STRAIN=BA1B/C; | |
| RX | Nuclein-94309676; PubMed=8035830; | |
| RA | Nuchprayoon I., Meyers S., Scott L.M., Suzow J., Hiebert S., | |
| RA | Friedman A.D.; | |
| RT | "PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2 | |
| RT | beta/CBF beta proto-oncoproteins, regulates the murine myeloperox- | |
| RT | and neutrophil elastase genes in immature myeloid cells.;" | |
| RL | Mol. Cell. Biol. 14:5558-5568(1994). | |
| CC | !- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY. | |

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2001, 06:10:39 ; Search time 16.8 Seconds
(without alignments)
811.928 Million cell updates/sec

Title: US-09-559-764-1

Perfect score: 1198

Sequence: 1 IVGGRKARPPFLASTQN.....VALFRDWDGVLNPNPGPPA 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

T number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

| | |
|-----|--|
| 1: | /SIDSL1/gcgdata/geneseq/geneseq/AA1980.DAT.* |
| 2: | /SIDSL1/gcgdata/geneseq/geneseq/AA1981.DAT.* |
| 3: | /SIDSL1/gcgdata/geneseq/geneseq/AA1982.DAT.* |
| 4: | /SIDSL1/gcgdata/geneseq/geneseq/AA1983.DAT.* |
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| 20: | /SIDSL1/gcgdata/geneseq/geneseq/AA1999.DAT.* |
| 21: | /SIDSL1/gcgdata/geneseq/geneseq/AA2000.DAT.* |
| 22: | /SIDSL1/gcgdata/geneseq/geneseq/AA2001.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query No. | Score | Match | Length | ID | Description |
|------------|-----------|-------|-------|--------|----------|--------------------|
| 1 | 1198 | 100.0 | 225 | 20 | AA121551 | Human heparin-bind |
| 2 | 1198 | 100.0 | 225 | 20 | AAW88118 | Mature human hepar |
| 3 | 1198 | 100.0 | 225 | 20 | AAW88362 | Human mature hepar |
| 4 | 1198 | 100.0 | 225 | 21 | AA171876 | Human mature hepar |
| 5 | 1198 | 100.0 | 225 | 22 | AA171891 | Human mature hepar |
| 6 | 1198 | 100.0 | 232 | 20 | AA121550 | Human heparin-bind |
| 7 | 1198 | 100.0 | 232 | 20 | AAW88120 | Human heparin-bind |
| 8 | 1198 | 100.0 | 232 | 20 | AAW88364 | Human pro-heparin |
| 9 | 1198 | 100.0 | 232 | 21 | AA171877 | Human pre-heparin |
| 10 | 1198 | 100.0 | 244 | 22 | AA171893 | Human preheparin-b |
| 11 | 1198 | 100.0 | 251 | 12 | AAR10668 | Cationic granule p |

| | | | | | | |
|----|-------|-------|-----|----|----------|--------------------|
| 12 | 1198 | 100.0 | 251 | 16 | AA184666 | Human heparin-bind |
| 13 | 1198 | 100.0 | 251 | 20 | AAW88365 | Human prepro-hepar |
| 14 | 1198 | 100.0 | 251 | 21 | AA171878 | Human pre-pro hepa |
| 15 | 1198 | 100.0 | 251 | 22 | AA171894 | Human preprohepari |
| 16 | 1192 | 99.5 | 225 | 21 | AA171881 | Human heparin bind |
| 17 | 1190 | 99.3 | 225 | 21 | AA171883 | Human heparin bind |
| 18 | 1183 | 98.7 | 225 | 21 | AA171882 | Human heparin bind |
| 19 | 1181 | 98.6 | 222 | 14 | AA173210 | Recombinant cation |
| 20 | 1176 | 98.2 | 222 | 16 | AAW84665 | CAP37 protein. HO |
| 21 | 1174 | 98.0 | 274 | 16 | AAW88121 | Human heparin-bind |
| 22 | 1173 | 97.9 | 221 | 16 | AAW84663 | Complete human hep |
| 23 | 1161 | 96.9 | 221 | 17 | AAW04875 | Human heparin-bind |
| 24 | 1161 | 96.9 | 221 | 17 | AAW04875 | Heparin binding pr |
| 25 | 930 | 77.6 | 197 | 10 | AA191931 | Cationic granule p |
| 26 | 919.5 | 76.8 | 226 | 12 | AAR10669 | Porcine heparin-bi |
| 27 | 772 | 64.4 | 239 | 20 | AA121552 | Porcine heparin-bi |
| 28 | 772 | 64.4 | 239 | 20 | AAW88122 | Porcine heparin-bi |
| 29 | 772 | 64.4 | 239 | 20 | AAW88366 | Porcine preheparin |
| 30 | 772 | 64.4 | 239 | 22 | AA171895 | Porcine preheparin |
| 31 | 772 | 64.4 | 246 | 20 | AA121553 | Complete porcine h |
| 32 | 772 | 64.4 | 246 | 20 | AAW88123 | Pig prepro-heparin |
| 33 | 772 | 64.4 | 246 | 22 | AAW88367 | Complete porcine h |
| 34 | 772 | 64.4 | 246 | 22 | AA171896 | Porcine preprohepa |
| 35 | 766 | 63.9 | 219 | 17 | AAW04876 | Heparin binding pr |
| 36 | 765 | 63.9 | 219 | 16 | AAW84664 | Porcine heparin-bi |
| 37 | 761.5 | 63.6 | 221 | 20 | AAW88119 | Mature porcine-hep |
| 38 | 761.5 | 63.6 | 221 | 20 | AAW88363 | Pig mature heparin |
| 39 | 761.5 | 63.6 | 221 | 22 | AA171892 | Porcine mature hep |
| 40 | 753 | 62.9 | 217 | 10 | AA190806 | Porcine heparin bi |
| 41 | 500 | 41.7 | 247 | 22 | AA155525 | Human elastase var |
| 42 | 500 | 41.7 | 267 | 9 | AA180335 | Sequence of serine |
| 43 | 500 | 41.7 | 267 | 19 | AAW64262 | Human neutrophil e |
| 44 | 482.5 | 40.3 | 265 | 11 | AAW08269 | Mouse serine prote |
| 45 | 482.5 | 40.3 | 265 | 19 | AAW70534 | Mouse neutrophil e |

ALIGNMENTS

RESULT 1

AA121551

ID AA121551 standard; Protein; 225 AA.

AC AA121551;

XX

XX

DT 03-AUG-1999 (first entry)

XX

XX Human heparin-binding protein (HBP) signal, pro and mature sequence.

DE

XX Heparin-binding protein; HBP; apoptosis; Islets of Langerhans; beta cell; endothelial cell; nerve cell; azurophil granule; chemoattractant; cancer; polymorphonuclear leukocyte; monocyte; neurodegenerative disorder; human; neuromuscular disorder; human immunodeficiency virus; ischemic stroke; proteoglycan; mitochondrial matrix targeting protein; viral infection; apoptosis inhibitor; immune-mediated glomerulonephritis.

XX Homo sapiens.

OS

XX

XX W0926647-A1.

PN

XX

PD 03-JUN-1999.

XX

XX 20-NOV-1998; 98WO-DK00510.

XX

XX 03-DEC-1997; 97DK-0001394.

PR

XX 20-NOV-1997; 97DK-0001324.

XX

XX (NOVO) NOVO-NORDISK AS.

PA

XX Flodgaard HJ;

PI

XX WPI; 1999-347615/29.

DR

DR N-PSDB; AAX60695.

XX Modulating or decreasing apoptosis in cells useful for treating
PT neurodegenerative disorders and neuromuscular disorders
XX Claim 4, 5; Page 12; 74pp; English.
XX The invention relates to a new method of modulating or decreasing
CC apoptosis in mammalian beta cells of islets of Langerhans, endothelial
CC cells or nerve cells. The method comprises administering a mammalian
CC heparin-binding protein (HBP) which in a glycosylated form has: (i) a
CC molecular weight of 28 kDa; (ii) is produced in the azurophilic granules
CC of polymorphonuclear leukocytes; and (iii) is a chemoattractant for
CC monocytes. The new protein is useful for preventing or treating a
CC disorder (preferably in human patients) resulting from apoptosis of
CC mammalian cells, including insufficient functioning of insulin production
CC or insulin action, a neurodegenerative disorder, a neuromuscular
CC disorder, human immunodeficiency virus and ischemic stroke. Compositions
CC (a) comprising HBP and a proteoglycan which binds the HBP; and (b)
CC comprising the HBP and a protein which binds to the HBP are useful for
CC matrix targeting protein and which binds to the HBP are useful for
CC modulating or decreasing apoptosis in mammalian beta cells of islets of
CC Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,
CC the new apoptosis inhibitor does not cause disorders associated with the
CC inhibition of apoptosis such as cancer, autoimmune disorders such as
CC systemic lupus erythematosus, immune-mediated glomerulonephritis, and
CC viral infections. The present sequence represents the human HBP
CC signal sequence, prosequence and the mature sequence.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARQPFPLASIQNGRHFCGGLIHAFVMTAASCFSQSNPGVSTVVLGAYDL 60
DB 1 IVGGRKARQPFPLASIQNGRHFCGGLIHAFVMTAASCFSQSNPGVSTVVLGAYDL 60
QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLDMLLQLDREALTSSVTILPLQNAATVEAG 120
DB 61 RRRERQSRQTFSSISMSSENGYDPOQNLDMLLQLDREALTSSVTILPLQNAATVEAG 120
QY 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
DB 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
QY 181 CEGLAGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPA 225
DB 181 CEGLAGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPA 225

RESULT 2
AAW88118
ID AAW88118 standard; protein; 225 AA.
XX
AC AAW88118;
XX
DT 27-APR-1999 (first entry)
DE Mature human heparin-binding protein.
XX
KW Human; heparin-binding; azurophilic granules; polymorphonuclear leukocyte;
KW chemoattractant; antimicrobial; monocyte macrophage;
KW thrombospondin secretion.
XX
OS Homo sapiens.
XX WO9900417-A1.
XX 07-JAN-1999.
XX 22-JUN-1998; 98WO-DK00275.

XX 22-AUG-1997; 97DK-0000963.
PR 25-JUN-1997; 97US-0082413.
PR 30-JUN-1997; 97DK-0000773.
PR 11-AUG-1997; 97US-0055192.
XX (NOVO) NOVO-NORDISK AS.
PA Bjorn SE, Flodgaard HJ, Rasmussen PB, Svendsen I;
PI Wiberg FC;
XX WPI; 1999-095680/08.
DR N-PSDB; AAX04857.
XX Recombinant eukaryotic cells expressing mammalian heparin binding
PT protein in a mature form - useful as an antimicrobial, a regulator
PT of macrophage or monocyte function, and as a stimulant for monocyte
PT survival
XX Claim 14; Page 7; 59pp; English.
XX The heparin-binding protein is produced by azurophilic granules of
CC polymorphonuclear leukocytes and is a chemoattractant for monocytes.
CC The heparin-binding protein: has antimicrobial activity; regulates
CC monocyte/macrophage function (chemotaxis, survival and differentiation);
CC mediates detachment and contraction of endothelial cells and fibroblasts
CC in monolayer cultures; and stimulates monocyte survival and
CC thrombospondin secretion.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARQPFPLASIQNGRHFCGGLIHAFVMTAASCFSQSNPGVSTVVLGAYDL 60
DB 1 IVGGRKARQPFPLASIQNGRHFCGGLIHAFVMTAASCFSQSNPGVSTVVLGAYDL 60
QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLDMLLQLDREALTSSVTILPLQNAATVEAG 120
DB 61 RRRERQSRQTFSSISMSSENGYDPOQNLDMLLQLDREALTSSVTILPLQNAATVEAG 120
QY 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
DB 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
QY 181 CEGLAGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPA 225
DB 181 CEGLAGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPA 225

RESULT 3
AAW88362
ID AAW88362 standard; protein; 225 AA.
XX
AC AAW88362;
XX
DT 26-APR-1999 (first entry)
DE Human mature heparin binding protein.
XX
KW Heparin binding protein; HBP; human; pathogen; Mycobacterium;
KW Listeria; Leishmania; HIV; infection; therapy; mononuclear cell;
KW monocyte; macrophage.
XX
OS Homo sapiens.
XX WO9900416-A1.
XX 07-JAN-1999.

PF 22-JUN-1998; 98WO-DK00274.
 XX 22-AUG-1997; 97DK-0000962.
 PR 25-JUN-1997; 97US-0050787.
 PR 30-JUN-1997; 97DK-0000772.
 PR 11-AUG-1997; 97US-0055191.
 XX (NOVO) NOVO-NORDISK AS.
 PA Flodgaard HJ, Rasmussen PB;
 XX WPI; 1999-095679/08.
 PI N-PSDB; AAX06763.
 XX Inhibiting pathogen entry into mononuclear cells using
 XX heparin-binding protein: useful to treat diseases caused by
 PT intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium
 PT tuberculosis or human immunodeficiency virus
 XX Claim 15; Page 29-30; 57pp; English.
 XX This polypeptide comprises human mature heparin binding protein
 CC (HBP). A novel method for inhibiting entry of a pathogen into
 CC mononuclear cells of a patient comprises administering a
 CC pharmaceutical composition comprising a carrier or diluent and a
 CC mammalian HBP, especially a human or porcine HBP (see also AAW88363)
 CC which, in glycosylated form: (i) has mol.wt. of approximately 28
 CC kDa as determined by SDS-PAGE under reducing conditions; (ii) is
 CC produced in the azurophilic granules of polymorphonuclear leukocytes;
 CC and (iii) is a chemotactant for monocytes. The method is useful
 CC for inhibiting the entry of pathogens such as protozoa (especially
 CC Leishmania), bacteria (especially Listeria or Mycobacterium e.g.
 CC Mycobacterium tuberculosis) and viruses (especially HIV) into
 CC mononuclear cells, especially monocytes or macrophages in humans or
 CC pigs. It may also be used to treat diseases caused by intracellular
 CC pathogens.
 XX Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 1198; DB 20; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPRQFPFLASIQNGRHFGGALIHARFVMTAASCFSQNGPSTVVLGAYDL 60
 DB 1 ivggrkarprqfpflasiqngrhfgcgali harfvmtaascfsgnpgvstvvlgaydl 60
 QY 61 RRRERQSRQTFSTSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAIVEAG 120
 DB 61 rrrerqsrqtfsissmsengydpqnlndmlqlldreanltssvtlplqlnatveag 120
 QY 121 TRCQVAGWSQSGRLSRFRFVNVTVPEDQCRPNNVCTGVLTRRGGICNGDGTPLV 180
 DB 121 trcqvagwsgsgrlsrfrfvnvtvtpedqcrpnncvtgvltrrrggicngdgtplv 180
 QY 181 CEGLAHGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPPA 225
 DB 181 ceglahgvasfslgpcgrgdpdffttrvalfrdwidgvlvlnppgppa 225
 RESULT 4
 AAY71876
 ID AAY71876 standard; Protein; 225 AA.
 AC AAY71876;
 XX 26-MAR-2001 (first entry)
 DT Human mature heparin binding protein (HBP).
 DE Human; heparin binding protein; HBP; antiinflammatory; cardiovascular;
 XX immunosuppressive; vasotropic; prevention; treatment; bradykinin;
 KW

KW aprotinin; H-kininogen; systemic inflammatory response syndrome;
 KW pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
 KW adult respiratory distress syndrome; chemoattractant; inflammation;
 XX vascular damage.
 OS Homo sapiens.
 XX WO2000066151-A1.
 PN 09-NOV-2000.
 PD 28-APR-2000; 2000WO-DK00213.
 PF 29-APR-1999; 99US-0132748.
 PR 06-MAY-1999; 99DK-0000613.
 PR 01-OCT-1999; 99DK-0001402.
 PR 01-OCT-1999; 99US-0157384.
 XX (NOVO) NOVO NORDISK AS.
 PA Flodgaard HJ, Lindbom L, Bjorn S;
 XX WPI; 2000-687445/67.
 PI N-PSDB; AAD01922.
 XX Treating systemic inflammatory response syndrome, ischaemia reperfusion,
 PT anaphylaxis and allograft rejection by modulating release of bradykinin
 PT -
 XX Disclosure; Page 9; 75pp; English.
 XX The present sequence is a mature heparin binding protein (HBP) from
 CC human. HBP is a proteolytically inactive protein and is stored in
 CC the azurophilic granules of polymorphonuclear leukocytes. It induces
 CC contraction in the endothelial cells and fibroblasts. It serves as
 CC a chemoattractant for monocytes and/or activates them and is involved
 CC in the progression of inflammation. HBP serves as the signalling link
 CC in neutrophil induced vascular damage and activation of contact phase
 CC system with concomitant formation of bradykinin. It specifically plays a
 CC role in the pre-kallikrein (PK) mediated cleavage of H-kininogen (HK) to
 CC obtain the bradykinin sequence. The antagonists of HBP (e.g. aprotinin)
 CC decrease the permeability of the endothelial cells and are used to
 CC prevent or treat disorders resulting from the release of bradykinin
 CC such as systemic inflammatory response syndrome, ischaemia reperfusion,
 CC anaphylaxis and/or allograft rejection. They are also used to treat
 CC adult respiratory distress syndrome.
 XX Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 1198; DB 21; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPRQFPFLASIQNGRHFGGALIHARFVMTAASCFSQNGPSTVVLGAYDL 60
 DB 1 ivggrkarprqfpflasiqngrhfgcgali harfvmtaascfsgnpgvstvvlgaydl 60
 QY 61 RRRERQSRQTFSTSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAIVEAG 120
 DB 61 rrrerqsrqtfsissmsengydpqnlndmlqlldreanltssvtlplqlnatveag 120
 QY 121 TRCQVAGWSQSGRLSRFRFVNVTVPEDQCRPNNVCTGVLTRRGGICNGDGTPLV 180
 DB 121 trcqvagwsgsgrlsrfrfvnvtvtpedqcrpnncvtgvltrrrggicngdgtplv 180
 QY 181 CEGLAHGVASFSLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPPA 225
 DB 181 ceglahgvasfslgpcgrgdpdffttrvalfrdwidgvlvlnppgppa 225
 RESULT 5
 AAY71891

ID XX AAY71891 standard; Protein; 225 AA.
AC AAY71891;
XX
XX 26-MAR-2001 (first entry)
DT
XX Human mature heparin-binding protein (HBP).
DE
XX Human; heparin-binding protein; HBP; chemoattractant; monocyte;
KW thrombospondin; fibroblast; endothelial cell.
XX
OS Homo sapiens.
XX
XX WO200066627-A1.
PN
XX 09-NOV-2000.
PD
XX 28-APR-2000; 2000WO-DK00216.
PF
XX 29-APR-1999; 99US-0131574.
PR 26-MAY-1999; 99DK-0000612.
XX
XX (NOVO) NOVO NORDISK AS.
PA
XX Flodgaard HJ, Rasmussen PB, Bjorn S, Svendsen I;
PI
XX WPI; 2001-015973/02.
DR N-PSDB; AAD01931.
XX
XX Producing mammalian heparin-binding proteins to mediate detachment and
PT contraction of endothelial cells and fibroblasts, involves introducing
PT genes encoding heparin-binding proteins into mammalian cells and
PT culturing -
XX
XX Claim 5; Page 4; 44pp; English.
PS
XX The invention relates to a method for producing heparin-binding
CC protein (HBP) in a mammalian cell that can be cultured under
CC anaerobic conditions and involves introducing a gene encoding HBP into
CC mammalian cells, culturing the cell under conditions conducive to
CC expression of HBP, and recovering HBP from the culture medium. This
CC method is useful for producing HBP in recombinant mammalian cells.
CC The present sequence is mature human heparin-binding protein (HBP).
CC HBP is a proteolytically inactive protein stored in the
CC azurophilic granules of polymorphonuclear leukocytes. HBP functions
CC as a chemoattractant for monocytes. HBP is used to mediate
CC detachment and contraction of endothelial cells and fibroblasts when
CC added to cells grown in monolayer culture. HBP is also used to
CC stimulate monocyte survival and thrombospondin secretion.
XX
XX Sequence 225 AA;
SQ
Query Match 100.0%; Score 1198; DB 22; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.9e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARVMTAASCFCQSQNPGVSTVVLGAYDL 60
DB 1 ivggrkarprqfplasiqnggrhfcgcaliharvmtaascfcqsqnpvgstvtvlgaydl 60
QY 61 RRRERQSRGTFTSISSMSSENGYDPOQNLNDLMLIQ
DB 61 rrrerqsrqftrftssmssengydpqnlndlmlilq
QY 121 TRCQVAGWGSQRSLRPRFNVTVTPEDOC
DB 121 trcqvagwgsqrsgrslrprfnvntvtpedoc
QY 181 CEGLAHVASFSLGPCRGDPDFTRVALFRDWID
DB 181 ceglahvasfslgpcrgdpdfttrvalfrdwid

RESULT 6
AAY21550
ID AAY21550 standard; Protein; 232 AA.
XX
XX AC AAY21550;
XX
XX 03-AUG-1999 (first entry)
DT
XX Human heparin-binding protein (HBP) pro and mature sequence.
DE
XX Heparin-binding protein; HBP; apoptosis; Islets of Langerhans; beta cell;
KW endothelial cell; nerve cell; azurophilic granule; chemoattractant; cancer;
KW polymorphonuclear leukocyte; monocyte; neurodegenerative disorder; human;
KW neuromuscular disorder; human immunodeficiency virus; ischemic stroke;
KW proteoglycan; mitochondrial matrix targeting protein; viral infection;
KW apoptosis inhibitor; immune-mediated glomerulonephritis.
XX
XX Homo sapiens.
OS
XX WO9926647-A1.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-DK00510.
PF
XX 03-DEC-1997; 97DK-0001394.
PR 20-NOV-1997; 97DK-0001324.
XX
XX (NOVO) NOVO-NORDISK AS.
PA
XX Flodgaard HJ;
PI
XX WPI; 1999-347615/29.
DR N-PSDB; AAX60694.
XX
XX Modulating or decreasing apoptosis in cells useful for treating
PT neurodegenerative disorders and neuromuscular disorders
PT
XX Claim 4, 5; Page 11-12; 74pp; English.
XX The invention relates to a new method of modulating or decreasing
CC apoptosis in mammalian beta cells of Islets of Langerhans, endothelial
CC cells or nerve cells. The method comprises administering a mammalian
CC heparin-binding protein (HBP) which in a glycosylated form has: (i) a
CC molecular weight of 28 kDa; (ii) is produced in the azurophilic granules
CC of polymorphonuclear leukocytes; and (iii) is a chemoattractant for
CC monocytes. The new protein is useful for preventing or treating a
CC disorder (preferably in human patients) resulting from apoptosis of
CC mammalian cells, including insufficient functioning of insulin production
CC or insulin action, a neurodegenerative disorder, a neuromuscular
CC disorder, human immunodeficiency virus and ischemic stroke. Compositions
CC (a) comprising HBP and a proteoglycan which binds the HBP; and (b)
CC comprising the HBP and a protein which is a mammalian mitochondrial
CC matrix targeting protein and which binds to the HBP are useful for
CC modulating or decreasing apoptosis in mammalian beta cells of Islets of
CC Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,
CC the new apoptosis inhibitor does not cause disorders associated with the
CC inhibition of apoptosis such as cancer, autoimmune disorders such as
CC systemic lupus erythematosus, immune-mediated glomerulonephritis, and
CC viral infections. The present sequence represents the human HBP
CC prosequence and the mature sequence.
XX
XX Sequence 232 AA;
SQ
Query Match 100.0%; Score 1198; DB 20; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.9e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARVMTAASCFCQSQNPGVSTVVLGAYDL 60
DB 8 ivggrkarprqfplasiqnggrhfcgcaliharvmtaascfcqsqnpvgstvtvlgaydl 67

| | | | |
|----------|--|--|-----|
| Db | 8 | ivggrkarprgfflaiaqngqhrfeggaliharfvmtaascfsgqpvgstvtvlgaydl | 67 |
| QY | 61 | RRRRQSRQTESISSMSSENGYDPQQNLNDMLQLDREANTSSVTILPLQNAIVEAG | 120 |
| Db | 68 | rrrrrqrqtisissmsengydpqqnlndmlqlldreantssvtilplqnatveag | 127 |
| QY | 121 | TRCQVAGSGSORSGRLSRPRFVNVTVPEDOCRPNNVCTGLTRGGICNGDGGTPLY | 180 |
| Db | 128 | trcqvagwsgsggrlsrprfvnvtvpdqcrpnnvctgvltrrggicngdggtply | 187 |
| QY | 181 | CEGLAHGVASFSLGCGRGDPDFFTRVALFRDWDIGVLLNNPGPGPA | 225 |
| Db | 188 | ceglahgvasfslgpcrgdpdfftrvalfrwdigvllnnpgppa | 232 |
| RESULT 8 | | | |
| AAW88364 | | | |
| XX | ID | AAW88364 standard; Protein: 232 AA. | |
| AC | AAW88364; | | |
| XX | DT | 26-APR-1999 (first entry) | |
| XX | | Human pro-heparin binding protein. | |
| XX | | Heparin binding protein; HBP; human; pathogen; Mycobacterium; | |
| KW | | Listeria; Leishmania; HIV; Infection; therapy; mononuclear cell; | |
| KW | | monocyte; macrophage. | |
| XX | | | |
| OS | | Homo sapiens. | |
| XX | | | |
| FH | Key | Location/Qualifiers | |
| FT | Peptide | 1..7 | |
| FT | | /note= "pro-peptide" | |
| FT | Protein | 8..232 | |
| FT | | /note= "mature HBP" | |
| XX | | | |
| PN | WO9900416-A1. | | |
| XX | | | |
| PD | 07-JAN-1999. | | |
| XX | | | |
| PF | 22-JUN-1998; 98WO-DK00274. | | |
| XX | | | |
| PR | 22-AUG-1997; 97DK-0000962. | | |
| PR | 25-JUN-1997; 97US-0050787. | | |
| PR | 30-JUN-1997; 97DK-0000772. | | |
| PR | 11-AUG-1997; 97US-0055191. | | |
| XX | | | |
| PA | (NOVO) NOVO-NORDISK AS. | | |
| XX | | | |
| XX | Flodgaard HJ, Rasmussen PB; | | |
| P1 | WPI; 1999-095679/08. | | |
| XX | N-PSDB; AAX06765. | | |
| DR | | | |
| DR | | | |
| XX | | | |
| PT | Inhibiting pathogen entry into mononuclear cells using | | |
| PT | heparin-binding protein - useful to treat diseases caused by | | |
| PT | intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium | | |
| PT | tuberculosis or human immunodeficiency virus | | |
| XX | | | |
| PS | Disclosure; Page 30-31; 57pp; English. | | |
| XX | | | |
| CC | This polypeptide comprises human heparin binding protein (HBP) | | |
| CC | pro-peptide and mature protein. A novel method for inhibiting | | |
| CC | entry of a pathogen into mononuclear cells of a patient comprises | | |
| CC | administering a pharmaceutical composition comprising a carrier or | | |
| CC | diluent and a mammalian HBP, especially a human or porcine mature | | |
| CC | HBP (see also AAW88362-63) which, in glycosylated form: (i) has | | |
| CC | mol wt. of approximately 28 kDa as determined by SDS-PAGE under | | |
| CC | reducing conditions; (ii) is produced in the azurophil granules of | | |
| CC | polymorphonuclear leukocytes; and (iii) is a chemoattractant for | | |
| CC | monocytes. The method is useful for inhibiting the entry of | | |
| CC | pathogens such as protozoa (especially Leishmania), bacteria | | |

CC (especially Listeria or Mycobacterium e. Mycobacterium
CC tuberculosis) and viruses (especially HIV) into mononuclear cells,
CC especially monocytes or macrophages in humans or pigs. It may also
CC be used to treat diseases caused by intracellular pathogens.
XX
SQ Sequence .232 AA;

Query Match 100.0%; Score 1198; DB 20; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.9e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGGLIHARVMTAAACFQSQNGVSNVLGAYDL 60
DB 8 IVGGRKARPPFPFLASIQNGRHFCGGLIHARVMTAAACFQSQNGVSNVLGAYDL 67
QY 61 RRRERQSRQTFSSISMSSENGYDQQNLNDMLLQREANLTSSVTILPLPLQNAVTEAG 120
DB 68 RRRERQSRQTFSSISMSSENGYDQQNLNDMLLQREANLTSSVTILPLPLQNAVTEAG 127
QY 121 TRCQVAGWSGSRGRLSRFPFVNVTVPEDQCRPNVCTGVLTRGGICNGDGGTPLV 180
DB 128 TRCQVAGWSGSRGRLSRFPFVNVTVPEDQCRPNVCTGVLTRGGICNGDGGTPLV 187
QY 181 CEGLAGHVASFSLGPGCGPDPFTRVALFRDWIDGLNNPQGP 225
DB 188 CEGLAGHVASFSLGPGCGPDPFTRVALFRDWIDGLNNPQGP 232

RESULT 9
AAV71877
ID AAV71877 standard; Protein; 232 AA.
XX AAV71877;
AC AAV71877;
XX
DT 26-MAR-2001 (first entry)
XX Human pre-heparin binding protein (HBP)
XX Human; heparin binding protein; HBP; an
KW immunosuppressive; vasotropic; preventi
KW aprotinin; H-kininogen; systemic infla
KW pre-kallikrein; ischaemia reperfusion;
KW adult respiratory distress syndrome; ch
KW vascular damage.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 21 /note= "Encoded by TC"
XX
XX PN WO200066151-A1.
XX
XX PD 09-NOV-2000.
XX
XX PF 28-APR-2000; 2000WO-DK00213.
XX
XX PR 29-APR-1999; 99US-0132748.
XX PR 06-MAY-1999; 99DK-0000613.
XX PR 01-OCT-1999; 99DK-0001402.
XX PR 01-OCT-1999; 99US-0157384.
XX
XX PA (NOVO) NOVO NORDISK AS.
XX
XX FI Flodgaard HJ, Lindbom L, Bjorn S;
XX
XX DR WPI; 2000-687445/67.
XX DR N-PSDB; AAD01923.
XX
XX PT creating systemic inflammatory response
XX anaphylaxis and allograft rejection by
XX

XX
PS
XX
CC The present sequence is a pre-heparin binding protein (HBP) from
CC human. This sequence contains a signal sequence and a mature HBP.
CC HBP is a proteolytically inactive protein and is stored in the
CC the azurophil granules of polymorphonuclear leucocytes. It induces
CC contraction in the endothelial cells and fibroblasts. It serves as
CC a chemoattractant for monocytes and/or activates them and is involved
CC in the progression of inflammation. HBP serves as the signalling link
CC in neutrophil induced vascular damage and activation of contact phase
CC system with concomitant formation of bradykinin. It specifically plays a
CC role in the pre-kallikrein (PK) mediated cleavage of H-kininogen (HK) to
CC obtain the bradykinin sequence. The antagonists of HBP (e.g. aprotinin)
CC decrease the permeability of the endothelial cells and are used to
CC prevent or treat disorders resulting from the release of bradykinin
CC such as systemic inflammatory response syndrome, ischaemia reperfusion,
CC anaphylaxis and/or allograft rejection. They are also used to treat
CC adult respiratory distress syndrome.
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 1198; DB 21; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.9e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGGLIHARVMTAAACFQSQNGVSNVLGAYDL 60
DB 8 IVGGRKARPPFPFLASIQNGRHFCGGLIHARVMTAAACFQSQNGVSNVLGAYDL 67
QY 61 RRRERQSRQTFSSISMSSENGYDQQNLNDMLLQREANLTSSVTILPLPLQNAVTEAG 120
DB 68 RRRERQSRQTFSSISMSSENGYDQQNLNDMLLQREANLTSSVTILPLPLQNAVTEAG 127
QY 121 TRCQVAGWSGSRGRLSRFPFVNVTVPEDQCRPNVCTGVLTRGGICNGDGGTPLV 180
DB 128 TRCQVAGWSGSRGRLSRFPFVNVTVPEDQCRPNVCTGVLTRGGICNGDGGTPLV 187
QY 181 CEGLAGHVASFSLGPGCGPDPFTRVALFRDWIDGLNNPQGP 225
DB 188 CEGLAGHVASFSLGPGCGPDPFTRVALFRDWIDGLNNPQGP 232

RESULT 10
AAV71893
ID AAV71893 standard; Protein; 244 AA.
XX
XX AC AAV71893;
XX
XX DT 26-MAR-2001 (first entry)
XX
XX DE Human preheparin-binding protein (HBP).
XX
XX KW Human; heparin-binding protein; HBP; chemoattractant; monocyte;
XX Thrombospondin; fibroblast; endothelial cell.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..244 /label= Mature_heparin_binding_protein
XX
XX PN WO200066627-A1.
XX
XX PD 09-NOV-2000.
XX
XX PF 28-APR-2000; 2000WO-DK00216.
XX
XX PR 29-APR-1999; 99US-0131574.
XX PR 06-MAY-1999; 99DK-0000612.

XX PA (NOVO) NOVO NORDISK AS.
 XX PI Flodgaard HJ, Rasmussen PB, Bjorn S, Svendsen I;
 XX PN WPI; 2001-015973/02.
 XX PD N-PSDB; AAD01933.
 XX PF Producing mammalian heparin-binding proteins to mediate detachment and
 XX PR contraction of endothelial cells and fibroblasts, involves introducing
 XX PT genes encoding heparin-binding proteins into mammalian cells and
 XX PS culturing.
 XX PS Disclosure; Page 6; 44pp; English.
 XX PI The invention relates to a method for producing heparin-binding
 XX CC protein (HBP) in a mammalian cell that can be cultured under
 XX CC anaerobic conditions involving introducing gene encoding HBP into
 XX CC mammalian cells, culturing the cell under conditions conducive to
 XX CC expression of HBP, and recovering HBP from the culture medium. This
 XX CC method is useful for producing HBP in recombinant mammalian cells.
 XX CC The present sequence is human heparin-binding
 XX CC protein (HBP) (which includes signal sequence and mature protein).
 XX CC HBP is a proteolytically inactive protein stored in the azurophil
 XX CC granules of polymorphonuclear leukocytes. HBP functions as a
 XX CC chemoattractant for monocytes. HBP is used to mediate detachment
 XX CC and contraction of endothelial cells and fibroblasts when added to
 XX CC cells grown in monolayer cultures. It is also used to stimulate
 XX CC monocyte survival and thrombospondin secretion.
 XX SQ Sequence 244 AA;
 Query Match 100.0%; Score 1198; DB 22; Length 244;
 Best Local Similarity 100.0%; Pred. No. 4.1e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPPFPFLASIQNGRHFCGGALIHARFVMTAASCFOQNPQGVSTVVLGAYDL 60
 DB 20 ivggrkarprqfpflasiqngqrhfcggalli harfvmtaascfqsqnpqgvstvlgaydl 79
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLMLQLDREANLTSSVTILPLQNAATVEAG 120
 DB 80 rrrerqsrqtfssmssengydpqgnlmlqldreanltssvtlplpqnatveag 139
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTPTDQCRPNNVCTGVLTRRGSGICNGDGTPLV 180
 DB 140 trcqvagwsqsggrslsrfvfnvvtptdqcrpnnvctgvltrrgsgicngdgtplv 199
 QY 181 CEGLAHGVASFSLGPGCGRGPDEFTRVALPRWDIDGVLNNGPGPA 225
 DB 200 ceglahgvasfslgpcgrgpdfttrvalfrwdidgvlwnpgpapa 244
 RESULT 11
 AAR10668
 ID AAR10668 standard; Protein; 251 AA.
 XX AC AAR10668;
 XX DT 17-APR-1991 (first entry)
 XX DE Cationic granule protein 37 sequence from clone 6a.1.
 XX KW Cationic granule protein 37; CAT37; polymorphonuclear leukocytes;
 XX KW PMN; lipopolysaccharide; LPS; wound healing; monocyte;
 XX KW chemoattractant.
 XX OS Homo sapiens.
 XX FT Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= sig_peptide

FT Protein 27..251
 FT /label= mat_protein
 XX W09100907-A.
 XX PD 24-JAN-1991.
 XX PF 03-JUL-1990; 90WO-US03772.
 XX PR 05-JUL-1989; 89US-0375739.
 XX PA (UYEM-) EMORY UNIV.
 XX PA (GENE-) GENELABS INC.
 XX PI Larrick JW, Morgan JG, Pereira HA, Spitznagel JK;
 XX WPI; 1991-051334/07.
 XX N-PSDB; AAQ10490.
 XX Recombinant DNA molecule encoding cationic granule protein -
 XX PT binds to Gram negative bacterial lipo:polysaccharide as monocyte
 XX PT chemoattractant, for treatment of wounds and monocyte disorders
 XX PS Disclosure; Page 82; 110pp; English.
 XX CC The mature form of CAP37 has an estimated mol.wt. of 24.276 kD.
 XX CC Previously Shafer et al. determined the mol.wt. to be 37 kD.
 XX CC This discrepancy is most likely the result of post-translational
 XX CC modification, e.g. glycosylation.
 XX CC The protein is a monocyte chemoattractant and can increase the
 XX CC migration of monocytes to a tissue site. It is therefore useful in
 XX CC wound healing, when used in a topical medication. It is useful for
 XX CC treating diseases involving monocyte localisation or defects of
 XX CC monocyte chemotaxis in an animal. The peptide can also be used for
 XX CC treating tumours of monocytes. The protein binds to bacterial LPS and
 XX CC therefore may provide an effective treatment for endotoxaemia.
 XX CC See also AAQ10490-95.
 XX SQ Sequence 251 AA;
 Query Match 100.0%; Score 1198; DB 12; Length 251;
 Best Local Similarity 100.0%; Pred. No. 4.2e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPPFPFLASIQNGRHFCGGALIHARFVMTAASCFOQNPQGVSTVVLGAYDL 60
 DB 27 ivggrkarprqfpflasiqngqrhfcggalli harfvmtaascfqsqnpqgvstvlgaydl 86
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLMLQLDREANLTSSVTILPLQNAATVEAG 120
 DB 87 rrrerqsrqtfssmssengydpqgnlmlqldreanltssvtlplpqnatveag 146
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTPTDQCRPNNVCTGVLTRRGSGICNGDGTPLV 180
 DB 147 trcqvagwsqsggrslsrfvfnvvtptdqcrpnnvctgvltrrgsgicngdgtplv 206
 QY 181 CEGLAHGVASFSLGPGCGRGPDEFTRVALPRWDIDGVLNNGPGPA 225
 DB 207 ceglahgvasfslgpcgrgpdfttrvalfrwdidgvlwnpgpapa 251
 RESULT 12
 AAR84666
 ID AAR84666 standard; Protein; 251 AA.
 XX AC AAR84666;
 XX DT 02-JUN-1996 (first entry)
 XX DE Human heparin-binding protein.
 XX KW Heparin-binding protein; Gram-negative sepsis; septic shock;

KW disseminated intravascular coagulation; meningococcal meningitis;
KW lipopolysaccharide-induced cytokine cascade; disease; prevention;
KW therapy; plasmid pKEN-1783; Spodoptera frugiperda.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /note= "signal peptide"
FT Peptide 20..26
FT Peptide /label= propeptide
FT Protein /note= "N-terminal extension"
FT Protein 27..251
FT Protein /note= "mature heparin-binding protein"
FT Protein 27..247
FT Protein /note= "heparin-binding protein of AAR84663"
XX
XX W09528949-A1.
XX
XX 02-NOV-1995.
XX
XX 17-MAR-1995; 95WO-DK00121.
XX
XX 21-DEC-1994; 94DK-0001452.
XX 21-APR-1994; 94DK-0000464.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Flodgaard HJH, Rasmussen PB;
PI N-PSDB; AAT05129.
XX
XX Heparin-binding protein (HBP) composition - for prevention and
PT treatment of sepsis and other conditions
XX
XX Disclosure; Fig 2; 48pp; English.
XX
XX The sequence represents the human heparin-binding protein (HBP)
CC which is expressed in Spodoptera frugiperda insect cells transformed
CC with plasmid pSX221. The cells are cultured in a suitable medium,
CC i.e. one containing a sulphated polysaccharide (heparin) immobilised
CC on an inert carrier (agarose), under conditions suitable for HBP
CC expression. The protein sequence represents mature HBP preceded by
CC an N-terminal extension. To facilitate production of mature HBP,
CC a preferred DNA encodes an N-terminally extended HBP including a
CC protease cleavage site located between the N-terminal extension and
CC the mature HBP coding sequence i.e. (Asp-Glu-Gly-Arg) (Factor-Xa). These
CC sites can be engineered into the DNA sequence (protein sequence position 26-27). HBP, or its
CC fragments, are used in a pharmaceutical composition for the
CC prevention or treatment of diseases associated with induction of the
CC cytokine cascade by glycosylated lipopolysaccharide, specifically
CC Gram-negative sepsis, septic shock, disseminated intravascular
CC coagulation or meningococcal meningitis.
XX
SQ Sequence . 251 AA;

Query Match 100.0%; Score 119; DB 16; Length 251;
Best Local Similarity 100.0%; Pred. No. 2e-89;
Matches 225; Conservative 0; Mismatches 0; Gaps 0;

QY 1 IVGGRKARQFFFLASTNQGRHFCGGLIHARMTAASCFQSQNPQGVSTVVLGAYDL 60
DB 27 ivggrkarqffflasiqngrrhfcggliahtmtaascfqsqnpqgvstvvlgaydl 86
QY 61 RRRERQRQRTFTSSSENQYDFQONLMLLQREANLTSVILPLPLQNATVEAG 120
DB 87 rrrerqrqrftssmsengdydpqgnindmlleareanltssvtlplplqnatveag 146
QY 121 TRCQVAGWSGRSGLSRPFRFVNVTVTPEDOCNNVCTGVLTTRGGICNGDGGTPLY 180
121 trcqvagwsgrsgrlspfrfvnvtvtpe
147 trcqvagwsgrsgrlspfrfvnvtvtpe
181 CEGLAHGVASFSLGCGRGPDPDFTRVALFRDWDIDGVLNNPQGP 225
207 ceglahgvasfslgpcgrgdpdftrvalfrdwdidgvlnnpgp 251
RESULT 13
AAW838365
ID AAW838365 standard; Protein; 251 AA.
XX
XX AAW838365;
XX
DT 26-APR-1999 (first entry)
XX
DE Human prepro-heparin binding protein.
XX
KW Heparin binding protein; HBP; human; pathogen; Mycobacterium;
KW Listeria; Leishmania; HIV; infection; therapy; mononuclear cell;
KW monocyte; macrophage.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /note= "signal peptide"
FT Peptide 20..26
FT Peptide /note= "pro-peptide"
FT Protein 27..251
FT Protein /note= "mature HBP"
XX
XX W09900416-A1.
XX
XX 07-JAN-1999.
XX
XX 22-JUN-1998; 98WO-DK00274.
XX
XX 22-AUG-1997; 97DK-0000962.
XX 25-JUN-1997; 97US-0050787.
XX 30-JUN-1997; 97DK-0000772.
XX 11-AUG-1997; 97US-0055191.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Flodgaard HJ, Rasmussen PB;
PI N-PSDB; AAX06766.
XX
XX Inhibiting pathogen entry into mononuclear cells using
XX heparin-binding protein - useful to treat diseases caused by
XX intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium
XX tuberculosis or human immunodeficiency virus
XX
XX Disclosure; Page : 57pp; English.
XX
XX This polypeptide comprises human heparin binding protein (HBP)
XX signal peptide, pro-peptide and mature protein. A novel method for
XX inhibiting entry of a pathogen into mononuclear cells of a patient
XX comprises administering a pharmaceutical composition comprising a
XX carrier or diluent and a mammalian HBP, especially a human or
XX porcine mature HBP (see also AAW8362-63) which, in glycosylated form:
XX (i) has a mol.wt. of approximately 28 kDa as determined by SDS-PAGE
XX under reducing conditions; (ii) is produced in the azurophilic granules
XX of polymorphonuclear leukocytes; and (iii) is a chemottractant for
XX monocytes. The method is useful for inhibiting the entry of
XX pathogens such as protozoa (especially Leishmania), bacteria
XX (especially Listeria or Mycobacterium e.g. Mycobacterium
XX tuberculosis) and viruses (especially HIV) into mononuclear cells,
XX especially monocytes or macrophages in humans or pigs. It may also
XX be used to treat diseases caused by intracellular pathogens.
XX (NB, the sequence of the signal and pro-peptide of human prepro-HBP
XX are not provided in the specification, but have been deduced from

CC the DNA sequence given in AAX06766).

XX Sequence 251 AA;

SQ

Query Match 100.0%; Score 1198; DB 20; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2e-89;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFCGALIHARFVMTAASCFQSQNGPVSTVVLGAYDL 60

DB 27 IVGGRKARPRQFPFLASIQNGRHFCGALIHARFVMTAASCFQSQNGPVSTVVLGAYDL 86

QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 120

DB 87 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 146

QY 121 TRCQVAGWSQSGRLSRFRFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180

DB 147 TRCQVAGWSQSGRLSRFRFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 206

QY 181 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 225

DB 207 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 251

RESULT 14

AAY71878

ID AAY71878 standard; Protein; 251 AA.

XX

AC AAY71878;

XX

DT 26-MAR-2001 (first entry)

XX

DE Human pre-pro heparin binding protein (HBP).

XX

KW Human; heparin binding protein; HBP; antiinflammatory; cardiovascular;

KW immunosuppressive; vasotropic; prevention; treatment; bradykinin;

KW aprotinin; H-kininogen; systemic inflammatory response syndrome;

KW pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;

KW adult respiratory distress syndrome; chemoattractant; inflammation;

KW vascular damage.

XX

OS Homo sapiens.

XX

PN WO200066151-A1.

XX

PP 09-NOV-2000.

XX

PR 28-APR-2000; 2000WO-DK00213.

XX

PR 29-APR-1999; 99US-0132748.

PR 06-MAY-1999; 99DK-0000613.

PR 01-OCT-1999; 99DK-0001402.

PR 01-OCT-1999; 99US-0157384.

XX

PA (NOVO) NOVO NORDISK AS.

XX

XX Flodgaard HJ; Lindbom L, Bjorn S;

XX

XX WPI: 2000-687445/67.

DR N-PSDB; AAD01924.

XX

XX Treating systemic inflammatory response syndrome, ischaemia reperfusion,

PT anaphylaxis and allograft rejection by modulating release of bradykinin

PT

XX

PS Disclosure; Page 13; 75pp; English.

XX

CC The present sequence is a human pre-pro heparin binding protein (HBP)

CC which contains a pro sequence, a signal sequence and a mature HBP

CC sequence. HBP is a proteolytically inactive protein and is stored in

CC the azurophil granules of polymorphonuclear leucocytes. It induces

CC contraction in the endothelial cells and fibroblasts. It serves as

CC a chemoattractant for monocytes and/or activates them and is involved

CC in the progression of inflammation. HBP serves as the signalling link

CC in neutrophil induced vascular damage and activation of contact phase

CC system with concomitant formation of bradykinin. It specifically plays a

CC role in the pre-kallikrein (PK) mediated cleavage of bradykinin. It specifically plays a

CC obtain the bradykinin sequence. The antagonists of HBP (e.g. aprotinin)

CC decrease the permeability of the endothelial cells and are used to

CC prevent or treat disorders resulting from the release of bradykinin

CC such as systemic inflammatory response syndrome, ischaemia reperfusion,

CC anaphylaxis and/or allograft rejection. They are also used to treat

CC adult respiratory distress syndrome.

XX

SQ Sequence 251 AA;

Query Match 100.0%; Score 1198; DB 21; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2e-89;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFCGALIHARFVMTAASCFQSQNGPVSTVVLGAYDL 60

DB 27 IVGGRKARPRQFPFLASIQNGRHFCGALIHARFVMTAASCFQSQNGPVSTVVLGAYDL 86

QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 120

DB 87 RRRERQSRQTFSSISMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 146

QY 121 TRCQVAGWSQSGRLSRFRFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180

DB 147 TRCQVAGWSQSGRLSRFRFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 206

QY 181 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 225

DB 207 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 251

RESULT 15

AAY71894

ID AAY71894 standard; Protein; 251 AA.

XX

AC AAY71894;

XX

DT 26-MAR-2001 (first entry)

XX

DE Human preproheparin-binding protein (HBP).

XX

KW Human; heparin-binding protein; HBP; chemoattractant; monocyte;

KW thrombospondin; fibroblast; endothelial cell.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..19 /label= Signal_peptide

FT Region 20..26 /note= "Pro-sequence of heparin-binding protein"

FT Protein 27..251 /label= Mature_heparin_binding_protein

XX

XX WO200066627-A1.

PN

XX

PD 09-NOV-2000.

XX

PF 28-APR-2000; 2000WO-DK00216.

XX

PR 29-APR-1999; 99US-0131574.

PR 06-MAY-1999; 99DK-0000612.

XX

PA (NOVO) NOVO NORDISK AS.

XX

XX Flodgaard HJ, Rasmussen PB, Bjorn S, Svendsen I;

XX

DR WPI: 2001-015973/02.
DR N-PSDB; AAD01934.
XX
PT Producing mammalian heparin-binding proteins to mediate detachment and
PT contraction of endothelial cells and fibroblasts, involves introducing
PT genes encoding heparin-binding proteins into mammalian cells and
PT culturing.
XX
PS Disclosure; Page 7; 44pp; English.
XX
CC The invention relates to a method for producing heparin-binding
CC protein (HBP) in a mammalian cell that can be cultured under
CC anaerobic conditions involves introducing a gene encoding HBP into
CC mammalian cells, culturing the cell under conditions conducive to
CC expression of HBP, and recovering HBP from the culture medium. This
CC method is useful for producing HBP in recombinant mammalian cells.
CC The present sequence is human heparin-binding protein, the pro sequence
CC and sequence of the mature protein).
CC HBP is a proteolytically inactive protein stored in the azurophil
CC granules of polymorphonuclear leucocytes. HBP functions as a
CC chemoattractant for monocytes. HBP is used to mediate detachment
CC and contraction of endothelial cells and fibroblasts when added to
CC cells grown in monolayer cultures. It is also used to stimulate
CC monocyte survival and thrombospondin secretion.
XX
SQ Sequence 251 AA;

Query Match 100.0%; Score 119; DB 22; Length 251;
Best Local Similarity 100.0%; Pred. NO. 2e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFFFLASIQNGRHFCGGALIHARMTAASCFOSONPGVSTVILGAYDL 60
Db 27 ivggrkarprqffflasiqngqrhfcggaliharmtaascfqsqnpqgvstvigaydl 86
QY 61 RRRERQSRQTFSTSSMSSENGYDPOQNLNDLMLIQREANLTSSVTILPLIQNATVEAG 120
Db 87 rrrerqsrqtffsissmsengydpqgnlndlmlqreanltssvtilpliqnatveag 146
QY 121 TRCOVAGWSQSGRLSRPRFVNVTVPEDOCNNVCTGVLTTRGGICNGDGGTPLY 180
Db 147 trcvagwsgsggrlsrprfvnvtvpedqcnnvctgvlttrggicngdggtply 206
QY 181 CEGLAHGVASFSLGCGRGPDFFTRVALFRWDIXVLNPPGPGPA 225
Db 207 ceglahgvasfslgpcgrgpdfftrvalfrwdixvlnppgpgpa 251

Search completed: November 23, 2001, 06:11:3
Job time: 53 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 23, 2001, 07:18:06 ; Search time 12.57 Seconds
(without alignments)
402.804 Million cell updates/sec

Title: US-09-559-764-1
Perfect score: 1198
Sequence: 1 IVGGRKARPRQPFPLASTQN.....VALFRDWTGVLNPNPGGPA 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1198 | 100.0 | 225 | 4 | US-08-944-483-32 |
| 2 | 1181 | 98.6 | 222 | 1 | US-07-969-931-9 |
| 3 | 1181 | 98.6 | 222 | 1 | US-07-855-417A-9 |
| 4 | 1176 | 98.2 | 222 | 2 | US-08-491-204A-18 |
| 5 | 1161 | 96.9 | 221 | 2 | US-08-925-708-1 |
| 6 | 766 | 63.9 | 219 | 2 | US-08-925-708-2 |
| 7 | 500 | 41.7 | 238 | 4 | US-08-944-483-31 |
| 8 | 500 | 41.7 | 238 | 6 | 5180819-4 |
| 9 | 500 | 41.7 | 267 | 2 | US-08-978-404B-46 |
| 10 | 476.5 | 39.8 | 229 | 2 | US-08-394-600B-20 |
| 11 | 476.5 | 39.8 | 229 | 4 | US-08-944-483-30 |
| 12 | 476.5 | 39.8 | 229 | 5 | PCT-US95-02513-20 |
| 13 | 476.5 | 39.8 | 256 | 2 | US-08-230-428B-4 |
| 14 | 434 | 36.2 | 214 | 6 | 5180819-3 |
| 15 | 417.5 | 34.8 | 215 | 6 | 5180819-2 |
| 16 | 333 | 27.8 | 234 | 4 | US-08-944-483-46 |
| 17 | 331 | 27.6 | 224 | 1 | US-08-278-091-12 |
| 18 | 331 | 27.6 | 224 | 1 | US-08-483-859-12 |
| 19 | 331 | 27.6 | 224 | 1 | US-08-472-173-12 |
| 20 | 331 | 27.6 | 224 | 2 | US-08-487-167-12 |
| 21 | 331 | 27.6 | 224 | 2 | US-08-482-816-12 |
| 22 | 331 | 27.6 | 224 | 2 | US-08-296-149-12 |
| 23 | 331 | 27.6 | 224 | 2 | US-08-801-499-12 |
| 24 | 331 | 27.6 | 224 | 2 | US-08-615-271-12 |
| 25 | 331 | 27.6 | 224 | 3 | US-09-074-660-12 |
| 26 | 331 | 27.6 | 224 | 3 | US-09-074-659-12 |
| 27 | 331 | 27.6 | 224 | 3 | US-09-106-468-12 |

28 331 27.6 224 4 US-09-106-466A-12
29 331 27.6 224 4 US-09-106-467-12
30 331 27.6 247 2 US-08-978-404B-47
31 329.5 27.5 232 4 US-08-944-483-45
32 325 27.1 223 6 5223425-8
33 325 27.1 260 6 5223425-10
34 323.5 27.0 259 6 5223425-2
35 322 26.9 228 4 US-08-944-483-44
36 321 26.8 238 6 5223425-5
37 321 26.8 250 6 5223425-4
38 318.5 26.6 235 2 US-08-557-146-14
39 318.5 26.6 235 2 US-09-154-344-14
40 318.5 26.6 235 4 US-08-944-483-42
41 318.5 26.6 225 1 US-08-344-483-42
42 315.5 26.3 223 1 US-07-956-848A-41
43 315.5 26.3 223 1 US-08-471-956-41
44 314.5 26.3 222 6 5223425-6
45 309 25.8 248 2 US-08-851-974-3

ALIGNMENTS

RESULT 1
US-08-944-483-32
; Sequence 32, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Sequence 12, Appl
Sequence 12, Appl
Sequence 47, Appl
Sequence 45, Appl
Patent No. 5223425
Patent No. 5223425
Patent No. 5223425
Patent No. 5223425
Sequence 14, Appl
Sequence 14, Appl
Sequence 42, Appl
Sequence 14, Appl
Sequence 41, Appl
Patent No. 5223425
Sequence 3, Appl



Matches' 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
 DB 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 DB 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
 DB 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
 QY 181 CEGLAGHVASFSLGPGCRGPDFFTRVALFRDWIDGVLNNPGP 222
 DB 181 CEGLAGHVASFSLGPGCRGPDFFTRVALFRDWIDGVLNNPGP 222

US-08-491-204A-18
 ; Sequence 18, Application US/08491204A
 ; Patent No. 5837247
 ; GENERAL INFORMATION:
 ; APPLICANT: Oppenheim, Joost B.
 ; APPLICANT: Chertov, Oleg
 ; APPLICANT: Michael, Dennis F.
 ; APPLICANT: Xu, Luoling
 ; APPLICANT: Wang, Ji Ming
 ; APPLICANT: Murphy, William J.
 ; APPLICANT: Longo, Dan L.
 ; APPLICANT: Taub, Dennis D.
 ; TITLE OF INVENTION: CHEMOTACTIC AGENTS FOR T-CELLS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491,204A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G15260
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORGANISM: human
 ; US-08-491-204A-18

Query Match 98.2%; Score 1176; DB 2; Length 222;
 Best Local Similarity 99.5%; Pred. No. 4.9e-116;
 Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60

DB 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 DB 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
 DB 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
 QY 181 CEGLAGHVASFSLGPGCRGPDFFTRVALFRDWIDGVLNNPGP 222
 DB 181 CEGLAGHVASFSLGPGCRGPDFFTRVALFRDWIDGVLNNPGP 222

RESULT 5
 US-08-925-708-1
 ; Sequence 1, Application US/08925708
 ; Patent No. 5939390
 ; GENERAL INFORMATION:
 ; APPLICANT: Flodgaard, Hans
 ; APPLICANT: Rasmussen, Poul Baad
 ; TITLE OF INVENTION: A Pharmaceutical Composition
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5939390o No. 5939390disk of No. 5939390th America, Inc.
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/925,708
 ; FILING DATE: 9-SEPT-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Agilis, Cheryl H.
 ; REGISTRATION NUMBER: 34,086
 ; REFERENCE/DOCKET NUMBER: 4319,204-US
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 221 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; US-08-925-708-1

Query Match 96.9%; Score 1161; DB 2; Length 221;
 Best Local Similarity 98.2%; Pred. No. 1.8e-114;
 Matches 217; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
 DB 1 IVGGRKARPPFPFLASIQNGRHFCCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 DB 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180

Db 121 TRCQVAGWSQSGRLSRFPBVBVTVPEDOCNNVCTGVLTRGGICNGDGGTPLV 180
QY 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDGLNNPG 221
Db 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDGLNNPG 221

RESULT 6
US-08-925-708-2
; Sequence 2, Application US/08925708
; Patent No. 5939390
; GENERAL INFORMATION:
; APPLICANT: Flogdaard, Hans
; APPLICANT: Rasmussen, Poul Baad
; TITLE OF INVENTION: A Pharmaceutical Composition
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59393900 No. 59393900 of No. 59393900th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,708
; FILING DATE: 9-SEPT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4319,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: porcine
; US-925-708-2

Query Match 63.9%; Score 766; DB 2; Length 219;
Best Local Similarity 67.7%; Pred. No. 2e-73;
Matches 149; Conservative 41; Indels 2; Gaps 2;

QY 1 IVGGRKARPPQFPFLASIQNGRHFCGCGALIHARVMTAASCFSQSNPGVSTVVLGAYDL 60
Db 1 IVGGRRAQPEPFLASIQKGRPFACAGLVHPRVLTAAACFRGKNGSGSASVVLGAYDL 60
QY 61 RRRERQSRQTSISSMSSENGYDPOONLNDMLLDREANLTSSVTILPLQNATVEAG 120
Db 61 RQOE-QSRQTSIRSISSQNGYDPRQNLNDVLLQDREARLTSPVALVPLPQBATVEAG 119
QY 121 TRCQVAGWSQSGRLSRFPBVBVTVPEDOCNNVCTGVLTRGGICNGDGGTPLV 180
Db 120 TRCQVAGWGTQRLRLSRFPBVBVTVPEDOCNNVCTGVLTRGGICNGDGGTPLV 178
QY 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDGLNNPG 220
Db 179 CNGLAGGVASFSLRRFRSSGFFTRVALFRDWIDGLNNPG 218

RESULT 7
US-08-944-483-31
; Sequence 31, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-31

Query Match 41.7%; Score 500; DB 4; Length 238;
Best Local Similarity 45.2%; Pred. No. 6.5e-45;
Matches 104; Conservative 36; Mismatches 82; Indels 8; Gaps 4;

QY 1 IVGGRKARPPQFPFLASIQNGRHFCGCGALIHARVMTAASCFSQSNPGVSTVVLGAYDL 60
Db 1 IVGGRRAQPEPFLASIQKGRPFACAGLVHPRVLTAAACFRGKNGSGSASVVLGAYDL 60
QY 61 RRRERQSRQTSISSMSSENGYDPOONLNDMLLDREANLTSSVTILPLQNATVEAG 120
Db 61 SRRE-PTROQFAVQRIFENGYPVNLNDIVILQNGSATINANVQVACLPAQGRRLNG 119
QY 121 TRCQVAGWSQSGRLSRFPBVBVTVPEDOCNNVCTGVLTRGGICNGDGGTPLV 180
Db 120 VQCLANGWGLLGRNGIASVLQELNVTVV-TSLCRRSNVCTILVRGQAGVCFDGSPLV 178
QY 181 CEGLAGHVASFSLGPCRG--PDFFTRVALFRDWIDGLV---NNPQGP 224
Db 179 CNGLIHGIAFVRGGCASGLYPDAFAPVQFVNWIDSIITORSIEDNPCHP 228

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;
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5968782e
; US-08-978-404B-46
;
; Query Match 41.7%; Score 500; DB 2; Length 267;
; Best Local Similarity 45.2%; Pred. No. 7.5e-45;
; Matches 104; Conservative 36; Mismatches 82; Indels 8; Gaps
;
QY 1 IVGGRKARPPFPELASTQNGRHFCGGALIHARVMTAASCFOSQNPGVSTVVLGAYDL 60
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 30 IVGGRARRAPHAWPFWLSQLRGGHFCGATLIAPNFVMSAAHCVANVRAVRVVLGAHNL 89
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 61 RRRERQSRQTSISSMSENGYDQQNLDMLLQLDREANLTSSVTILPLPLQNAATVEAG 120
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 90 SRRP-PTQQVFAVORIFENGYDVPNLLDIVILQNGSATINAVQVAQLPAQGRRLGNG 148
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 121 TRCQVAGRGSGRSGRLSRFPFVNVVTVPEDQCRPNNVCTGLVTRRGICNGDGCTPLV 180
Db :|| |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 149 VOCLAGMWGLGRNRGIIASVLQELNVTVV-TSLCRSNVCTLVRRQAGVCFGDSGSPLV 207
;
QY 181 CEGLAHGVASISLPCGRG--PDFFTRVALFRQWIDGVL---NNPGPGP 224
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
QY 208 CNGLIHGIASTRVGCASGLYPDAFAPVAFQFVNWIDSIQRSEDNPPCPHP 257
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
;
RESULT 10
; US-08-394-600B-20
; Sequence 20, Application US/08394600B
; Patent No. 5843693
;
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; APPLICANT: Jewell, David A.
; APPLICANT: Koths, Kirston E.
; APPLICANT: Kriegler, Michael
; APPLICANT: Perez, Carl
;
; TITLE OF INVENTION: Compositions for the Inhibition of
; TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street; 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,600B
; FILING DATE: 02/27/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donald J. Pochopien
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 820.005/11850US05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid

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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids

[illegible]

```

RESULT 14
5180819-3
; Patent NO. 5180819
; APPLICANT: INVENTOR, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455, 614
; FILING DATE: 22-DEC-1989
; SEQ ID NO:3:
; LENGTH: 214
5180819-3

```

| | Query Match | 36.2% | Score 434; | DB 6; | Length 214; |
|----|-----------------------|--|-------------------|----------------|----------------|
| | Best Local Similarity | 44.9%; | Pre. No. 4.9e-38; | | |
| | Matches 93; | Conservative | 36; | Mismatches 72; | Indels 6; Gaps |
| QY | 15 | LASIO---NCRHFCGGAITHAEVMTATASCFOSONPGYSTVVVLGAYDLRRERQSQTFF 71 | | | |
| Db | 1 | MASLOWRGNPCSHFCGGTLTHPFSVLTAACHLRDTPQLRVNVVLGAHNVRTOE-PTQQHF 59 | | | |
| QY | 72 | SISSENGSYDPQONLNDMLQLDRANLTSSVTITPLPLQNATEVAETRCQVAGWSQ 131 | | | |
| Db | 60 | SVAAQFELNNYAENKLANDILLIQLSSPANLSASVASVOLPQQDQPVPHGTCOLAMGWRY 119 | | | |
| QY | 132 | RSGGRLSRFPRFVNVTTPEDQCERNVCCTGYLTRGGTICNGDGGTPLVCEGLAHGVASF 191 | | | |
| Db | 120 | GHPDPAPVLOGLNTTV--TFCCRNINICTFVPRRKAGICFGDSGGPLICDGIITQGIDSF 178 | | | |
| QY | 192 | SLGPCGR-GPDFTRVALFRDWIDGVL 217 | | | |
| Db | 179 | IWGCATRLFPDFEFTRVALYVDWRSTLL 205 | | | |

Query Match 34.8%; Score 417.5; DB 6; Length 215;

Best Local Similarity 43.3%; Pred. No. 7e-36;
Matches 90; Conservative 37; Mismatches 74; Indels 7; Gaps 4;

QY 15 LASIQ---NQRHFCGALIHARFVMTAASCFS :||:| | ||| ||| ||:| | | :
Db 1 MASLOMRENPEHFCEETLIHPSFVLTAACHLRD : ||||:| | :| | :| |
QY 72 SISMSGENGYDPOONLNDMLLOLDREANLTSSV :||:| | |||:| | |||:| |
Db 60 SVAQVFLNNYDAENKLNLDILLIOLSSPANLSASV :||:| | |||:| | |||:| |
QY 132 RSGGRLSRFRPFVNVTVTPEDQCRPNNVCTGVLTF :||:| | |||:| | |||:| |
Db 120 GAHDPPAQVLQELNVTW-TFFCRPHNICTFVPR :||| | | ||:| | :| |
QY 192 SLGPCGRG--PDFFTRVALFRDWIDGVL 217 : | |||||:| | |
Db 179 VINGCATRLFPDFFTRVALYVDWIRSTL 206 : | |||||:| | |

Search completed: November 23, 2001, 07:18:20
Job time: 22 sec